

Sequence 14, Appl  
Sequence 14, Appl  
Patent No. 5168051  
Sequence 29, Appl  
Sequence 29, Appl  
Sequence 30, Appl  
Sequence 226, Appl  
Sequence 6, Appl  
Sequence 30, Appl  
Sequence 32, Appl  
Sequence 32, Appl  
Sequence 17, Appl  
Sequence 107, Appl  
Sequence 17, Appl  
Sequence 4, Appl  
Sequence 23, Appl  
Sequence 23, Appl

US-08-486-057B-11 10 1 US-08-486-057B-14  
Sequence 11, Application US/08486057B  
Patent No. 5650494  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5650494ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,057B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5650494ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

ALIGNMENTS

RESULT 1  
US-08-486-057B-11  
Sequence 11, Application US/08486057B  
Patent No. 5650494  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5650494ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,057B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5650494ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

28 56 34.4 10 1 US-08-486-057B-14  
29 56 34.4 10 2 US-08-789-588-14  
30 54 33.1 25 6 5168051-14  
31 50 30.7 9 1 US-08-486-057B-29  
32 50 30.7 9 2 US-08-789-588-29  
33 47 28.8 20 4 US-09-201-227A-30  
34 47 28.8 20 4 US-09-084-303B-226  
35 44 27.0 17 3 US-09-252-149B-6  
36 40 24.5 10 1 US-08-486-057B-30  
37 40 24.5 10 2 US-08-789-588-30  
38 38 23.3 9 1 US-08-486-057B-32  
39 38 23.3 9 2 US-08-789-588-32  
40 38 23.3 11 3 US-08-866-545-17  
41 38 23.3 11 4 US-09-428-082B-107  
42 38 23.3 11 4 US-09-627-775-17  
43 36 22.1 13 1 US-08-497-599-4  
44 36 22.1 13 2 US-08-486-057B-23  
45 36 22.1 13 2 US-08-789-588-23

ALIGNMENTS

RESULT 1  
US-08-486-057B-11  
Sequence 11, Application US/08486057B  
Patent No. 5650494  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5650494ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,057B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5650494ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	85.9	28	1	US-08-486-057B-11
2	140	85.9	28	2	US-08-789-588-11
3	130	79.8	29	1	US-08-486-057B-40
4	130	79.8	29	2	US-08-789-588-40
5	121	74.2	21	4	US-08-188-197-2
6	98	60.1	21	4	US-08-188-197-3
7	94	57.7	20	1	US-08-486-057B-36
8	94	57.7	20	2	US-08-789-588-36
9	92	56.4	21	4	US-08-188-197-4
10	78	47.9	16	1	US-08-009-448-4
11	78	47.9	16	1	US-08-400-607-4
12	77	47.2	19	1	US-08-486-057B-10
13	77	47.2	19	2	US-08-789-588-10
14	75	46.0	17	4	US-08-294-061-1
15	75	46.0	17	4	US-08-188-197-5
16	75	46.0	21	6	5168051-16
17	68	41.7	21	4	US-08-188-197-1
18	68	41.7	29	6	5262319-8
19	61	37.4	10	1	US-08-486-057B-17
20	61	37.4	10	2	US-08-789-588-17
21	61	37.4	16	1	US-08-009-448-3
22	61	37.4	16	1	US-08-400-607-3
23	60	36.8	13	1	US-08-486-057B-25
24	60	36.8	13	2	US-08-789-588-25
25	57	35.0	9	1	US-08-486-057B-15
26	57	35.0	9	2	US-08-789-588-15
27	57	35.0	13	6	5262319-3

LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-057B-11

Query Match 85.9%; Score 140; DB 1; Length 28;  
Best Local Similarity 92.9%; Pred. No. 2.1e-12;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRPLYIDFKRDL 28  
DB 1 ALDAAYCFRNVDNCCLRPLYIDFKRDL 28

## RESULT 2

US-08-789-588-11  
Sequence 11, Application US/08789588  
Patent No. 5922846

## GENERAL INFORMATION:

APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Henry P. No. 5922846ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789,588  
FILING DATE:

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,057  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5

FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5922846ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306

## SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-789-588-11

Query Match 85.9%; Score 140; DB 2; Length 28;  
Best Local Similarity 92.9%; Pred. No. 2.1e-12;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRPLYIDFKRDL 28  
DB 1 ALDAAYCFRNVDNCCLRPLYIDFKRDL 28

## RESULT 3

US-08-486-057B-40  
Sequence 40, Application US/08486057B  
Patent No. 5650494

## GENERAL INFORMATION:

APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Henry P. No. 5650494ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,057B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5

FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5650494ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306

## INFORMATION FOR SEQ ID NO: 40:

## SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-486-057B-40

Query Match 79.8%; Score 130; DB 1; Length 29;  
Best Local Similarity 89.7%; Pred. No. 5e-11;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

[REDACTED]

\_\_\_\_\_

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,197  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 22669J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-188-197-3

Query Match 60.1%; Score 98; DB 4; Length 21;  
Best Local Similarity 71.4%; Pred. No. 7.5e-07;  
Matches 15; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPYI 21  
DB 1 ALDTNYCFRNLNCCVRLPYI 21

RESULT 7  
US-08-486-057B-36  
Sequence 36, Application US/08486057B  
Patent No. 5650494  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5650494ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,057B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5650494ak, Henry P.

REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-057B-36

Query Match 57.7%; Score 94; DB 1; Length 20;  
Best Local Similarity 70.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 DAAAYCFRNVQDNCCLRLPYI 22  
DB 1 DTNYCFRNLNCCVRLPYI 20

RESULT 8  
US-08-789-588-36  
Sequence 36, Application US/08789588  
Patent No. 5922846  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5922846ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789,588  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,057  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5922846ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306

INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-789-588-36

Query Match 57.7%; Score 94; DB 2; Length 20;  
Best Local Similarity 70.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DAAYCFRNVDNCCRLPLYI 22  
Db 1 DTNYCFRNLENCVRLPLYI 20

RESULT 9  
US-08-188-197-4  
Sequence 4, Application US/08188197  
Patent No. 6586394  
GENERAL INFORMATION:  
APPLICANT: Iwata, Kenneth K.  
APPLICANT: Stephenson, John R.  
APPLICANT: Gold, Leslie I.  
TITLE OF INVENTION: TISSUE-DERIVED TUMOR GROWTH INHIBITORS,  
METHODS OF PREPARATION AND USES THEREOF  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,197  
FILING DATE: 27-JAN-1994

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 22669J  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-188-197-4

Query Match 56.4%; Score 92; DB 4; Length 21;  
Best Local Similarity 66.7%; Pred. No. 4.9e-06;  
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALDAAAYCFRNVDNCCRLPLYI 21  
Db 1 ALDNTNYCFRNLENCVRLPLYI 21

RESULT 10  
US-08-009-448-4  
Sequence 4, Application US/08009448

Patent No. 5420243  
GENERAL INFORMATION:  
APPLICANT: OGAWA, YASUSHI  
APPLICANT: SCHMIDT, DAVID  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE TGF-BETA1 AND  
TGF-BETA2 PEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/009,448  
FILING DATE: 19930126  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 22095-20007.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-009-448-4

Query Match 47.9%; Score 78; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00029;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CLRPLYIDFKRLDG 29  
Db 1 CLRPLYIDFKRLDG 14

RESULT 11  
US-08-400-607-4  
Sequence 4, Application US/08400607  
Patent No. 5658883  
GENERAL INFORMATION:  
APPLICANT: OGAWA, YASUSHI  
APPLICANT: SCHMIDT, DAVID  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE TGF-B1 AND TGF-B2  
PEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/400,607  
FILING DATE: 08-MAR-1995

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; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-057B-10

Query Match 47.2%; Score 77; DB 1; Length 19;
Best Local Similarity 84.2%; Pred No. 0.00047;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNVDNCCILRP 19
    ||||| ||||| |||
DB 1 ALDAAAYCFRNVDNXXILRP 19

RESULT 13
US-08-789-588-10
; Sequence 10, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; APPLICATION DATA: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid

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; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-10

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Query Match 47.2%; Score 77; DB 2; Length 19;  
Best Local Similarity 84.2%; Pred. No. 0.00047;  
Matches 16; Conservative 0; Mismatches 3; Indels

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Db 1 ALDAAYXFRNVQDXXLRP 19  
|||

RESULT 14  
US-08-294-061-1  
: Sequence 1, Application US/08294061

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/ / GENERAL INFORMATION:
/ / APPLICANT: Iwata, Kenneth K.
/ / APPLICANT: Stephenson, John R.
/ / APPLICANT: Gold, Leslie I.
/ / TITLE OF INVENTION: Tissue-Derived Tumor Growth
/ / TITLE OF INVENTION: Inhibitors,
/ / TITLE OF INVENTION: Methods of Preparation and Uses
/ / TITLE OF INVENTION: Thereof
/ / NUMBER OF SEQUENCES: 1
/ / CORRESPONDENCE ADDRESS:
/ / ADDRESSEE: Cooper & Dunham
/ / STREET: 30 Rockefeller Plaza
/ / CITY: New York
/ / STATE: New York
/ / COUNTRY: USA
/ / ZIP: 10112

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,661

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FILED DATE: 12/11/95  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 22669-K/JWP/NPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550

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/ INFORMATION FOR SEQ ID NO: 1:
/ =====
/ SEQUENCE CHARACTERISTICS:
/     LENGTH: 17 amino acids
/     TYPE: amino acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/     MOLECULE TYPE: peptide
/     HYPOTHETICAL: N
/     ANTI-SENSE: N
/     FRAGMENT TYPE: N-terminal
/     FEATURE:
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/ FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION:
US-08-294-061-1

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Query Match 46.0%; Score 75; DB 4; Length 17;  
Best Local Similarity 64.7%; Pred. No. 0.00078;  
Matches: 11: Conservative 4; Mismatches 2; Indels

Qy 1 ALDAA YCFRN VQDNCL 17  
||| ||| ::|||:  
Db 1 ALDTN YCFRN LEENC V 17

RESULT 15  
US-08-188-197-5 ; Sequence 5, Application US/08188137  
; Patent No. 6586394  
; GENERAL INFORMATION:  
; APPLICANT: Iwata, Kenneth K.  
; APPLICANT: Stephenson, John R.  
; APPLICANT: Gold, Leslie I.  
; TITLE OF INVENTION: TISSUE-DERIVED TUMOR GROWTH INHIBITORS,  
; TITLE OF INVENTION: METHODS OF PREPARATION AND USES THEREOF  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036

[illegible]

FILING DATE: 27-JAN-1994  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.

REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 22669J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525

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, INFORMATION FOR SEQ ID NO: 5:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 17 amino acids
, TYPE: amino acid
, STRANDEDNESS: single

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;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-08-188-197-5

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Query Match 46.0%; Score 75; DB 4; Length 17;  
Best Local Similarity 64.7%; Pred. No. 0.00078;  
Matches 11; Conservative 4; Mismatches 2; Indels

Qy 1 ALDAA YCFRNVDNCCL 17  
||| |||||::|||:  
Db 1 ALDTNYCFRNLEENC CV 17

Search completed: October 29, 2004, 08:42:05  
Job time : 38 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 08:22:38 ; Search time 190 Seconds  
(without alignments)

87.820 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAVCFERNQDNCCLREPLYIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	163	100.0	112	1	TGF2_BOVIN
2	163	100.0	224	2	Q8CDZ9
3	163	100.0	255	2	Q921T1
4	163	100.0	339	2	Q9EB7
5	163	100.0	412	1	TGF2_CHICK
6	163	100.0	414	1	TGF2_CERAE
7	163	100.0	414	1	TGF2_HUMAN
8	163	100.0	414	1	TGF2_MOUSE
9	163	100.0	414	2	Q91V5
10	163	100.0	435	1	TGF2_PIG
11	163	100.0	442	1	TGF2_RAT
12	163	100.0	442	2	Q6T7C3
13	163	100.0	442	2	AAR06973
14	160	98.2	413	1	TGF2_XENLA
15	148	90.8	361	2	Q98854
16	133	81.6	362	2	Q99K17
17	133	81.6	409	1	TGF3_PIG
18	133	81.6	410	1	TGF3_MOUSE
19	133	81.6	412	1	TGF3_HUMAN
20	133	81.6	412	1	TGF3_RAT
21	133	81.6	412	2	Q91Y07
22	124	76.1	411	2	Q7SZV4
23	119	73.0	91	2	Q9MYZ1
24	118	72.4	410	2	TGF3_CHICK
25	118	72.4	412	1	TGF3_MOUSE
26	113	69.3	179	2	Q90YF2
27	111	68.1	112	2	Q02730
28	111	68.1	124	2	Q95N80
29	111	68.1	130	2	Q08714
30	111	68.1	315	1	TGF1_BOVIN
31	111	68.1	368	2	Q8R4D9

32	111	68.1	390	1	TGF1_CANFA	P54831	canis famil
33	111	68.1	390	1	TGF1_CERAE	P09533	cercoptithec
34	111	68.1	390	1	TGF1_HORSE	O19011	equus cabal
35	111	68.1	390	1	TGF1_HUMAN	P01137	homo sapien
36	111	68.1	390	1	TGF1_MOUSE	P04202	mus muscucu
37	111	68.1	390	1	TGF1_PIG	P07200	sus scrofa
38	111	68.1	390	1	TGF1_RAT	P17246	rattus norv
39	111	68.1	390	1	TGF1_SHEEP	P50414	ovis aries
40	111	68.1	390	2	AAP35909	AAP35909	homo sapi
41	111	68.1	390	2	AAS55640	AAS55640	rattus no
42	107	65.6	390	1	TGF1_CAVPO	O921V6	cavia porce
43	104	63.8	86	2	Q28241	Q28241	cervus elap
44	103	63.2	390	2	Q9TUM8	Q9TUM8	equus cabal
45	97	59.5	127	2	Q9TV08	Q9TV08	canis famil

#### ALIGNMENTS

RESULT 1  
TGF2\_BOVIN  
ID TGF2\_BOVIN STANDARD; PRT; 112 AA.  
AC P21214;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Transforming growth factor beta 2 (TGF-beta 2) (Milk growth factor) (MGF).  
GN Name=TGFβ2;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Milk;  
RX MEDLINE=92189724; PubMed=1799413;  
RA Jin Y., Cox D.A., Knecht R., Raschdorf F., Cerletti N.,  
RT "Separation, purification, and sequence identification of TGF-beta 1 and TGF-beta 2 from bovine milk."  
RL J. Protein Chem. 10:565-575(1991).  
RN [2]  
RP SEQUENCE OF 1-30.  
RC TISSUE=Bone;  
RX MEDLINE=87137406; PubMed=3469199;  
RA Seyedin S.M., Segarini P.R., Rosen D.M., Thompson A.V., Bentz H.,  
RT "Cartilage-inducing factor-B is a unique protein structurally and functionally related to transforming growth factor-beta."  
RL J. Biol. Chem. 262:1946-1949(1987).  
RN [3]  
RP SEQUENCE OF 1-19.  
RC TISSUE=Milk;  
RX MEDLINE=91224126; PubMed=2026157;  
RA Cox D.A., David A., Buerk R.R.;  
RT "Isolation and characterization of milk growth factor, a transforming-growth-factor-beta 2-related polypeptide, from bovine milk."  
RL Eur. J. Biochem. 197:353-358(1991).  
RN [4]  
RP SUBUNITS.  
RC TISSUE=Bone;  
RX MEDLINE=92129307; PubMed=1733936;  
RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;  
RT "Purification and characterization of transforming growth factor-beta 2.3 and -beta 1.2 heterodimers from bovine bone."  
RL J. Biol. Chem. 267:2325-2328(1992).  
CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2 dependent T-cell growth.  
CC -!- SUBUNIT: Homodimer; disulfide-linked. Heterodimers of TGF-beta 1/2 and of TGF-beta 2/3 have been found in bone.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the TGF-beta family.

```

DR PIR; A61439; A61439.
DR HSP; P08112; 2TGI.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOR.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Direct protein sequencing; Growth factor; Milk; Mitogen.
KW DISULFID 7 16
FT DISULFID 15 78 By similarity.
FT DISULFID 44 109 By similarity.
FT DISULFID 48 111 By similarity.
FT DISULFID 77 77 Interchain (By similarity).
SQ SEQUENCE 112 AA; 12719 MW; 5142C7432C4EB1C CRC64;

Query Match 100.0%; Score 163; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAFCFRVQDNCCLRPYLIDFKRDLG 29
Db 1 ALDAAFCFRVQDNCCLRPYLIDFKRDLG 29

RESULT 2
Q8CDZ9 PRELIMINARY; PRT; 224 AA.
AC Q8CDZ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:483241A13 product:transforming growth factor, beta 2,
DE full insert sequence. (Fragment).
GN Name=Tgfb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai X., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AK029306; BAC26384.1; -.
DR MGI; MGI198726; Tgfb2.
DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR003940; TGFb2.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR01425; TGFb2.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
SQ SEQUENCE 224 AA; 25538 MW; 9264D6C878C8D2BC CRC64;
Query Match 100.0%; Score 163; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAFCFRVQDNCCLRPYLIDFKRDLG 29
Db 113 ALDAAFCFRVQDNCCLRPYLIDFKRDLG 141

RESULT 3
Q921T1 PRELIMINARY; PRT; 255 AA.
ID Q921T1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tgfb2 protein.
GN Name=Tgfb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RT TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Aramanci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Phney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Kzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N;  
RC TISSUE=Mammary tumor, Metastathionien-TGF alpha model. 10 month old  
RC virgin mouse. Taken by biopsy.;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
DR EMBL; BC011055; AAH11055.1; -;  
DR HSSP; P08112; 2TGI.  
DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.  
DR MGD; MGI:98726; Tgfb2.  
DR GO; GO:0002400; Gfysknot.  
DR InterPro; IPR002400; Tgfb.  
DR InterPro; IPR001839; Tgfb.  
DR InterPro; IPR003940; Tgfb2.  
DR InterPro; IPR001111; Tgfb N.  
DR InterPro; IPR003911; TGF Tgfb.  
DR Pfam; PF00688; Tgfb\_propeptide; 1.  
DR Pfam; PF00039; TGF\_beta; 1.  
DR PRINTS; PR01423; TGFbeta.  
DR PRINTS; PR01425; TGFbeta2.  
DR ProDom; PD000357; Tgfb; 1.  
DR SMART; SM00204; Tgfb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
RW Growth factor.  
XN NCBI\_TaxID=9031;  
SQ SEQUENCE 255 AA; 29087 MW; 94540017F3C5C219 CRC64;  
Query Match 100.0%; Score 163; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 9.4e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 29  
Db 144 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 172  
RESULT 4  
Q9ERB7 PRELIMINARY; PRT; 399 AA.  
AC Q9ERB7;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
CX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ramesh G., Kondaiah P., Seshagiri P.B.;  
Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
-!- SIMILARITY: Belongs to the TGF-beta family.  
DR HSSP; P08112; 2TGI.  
DR GO; GO:0008083; F:transforming growth factor beta receptor bi. . .; IEA.  
DR GO; GO:0005160; P:transforming growth factor beta receptor bi. . .; IEA.  
DR GO; GO:0016049; P:cell growth; IEA.  
DR InterPro; IPR001839; Tgfb.  
DR InterPro; IPR003940; Tgfb2.  
DR InterPro; IPR001111; Tgfb N.  
DR InterPro; IPR003911; TGF Tgfb.  
DR Pfam; PF00688; Tgfb\_propeptide; 1.  
DR Pfam; PF00039; TGF\_beta; 1.  
DR PRINTS; PR01423; TGFbeta.  
DR PRINTS; PR01425; TGFbeta2.  
DR ProDom; PD000357; Tgfb; 1.  
DR SMART; SM00204; Tgfb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
RW Growth factor.  
FT NON\_TER 1  
FT NON\_TER 399  
SQ SEQUENCE 399 AA; 46078 MW; A6FFB65EAFD5148 CRC64;  
Query Match 100.0%; Score 163; DB 2; Length 399;  
Best Local Similarity 100.0%; Pred. No. 1.4e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 29  
Db 296 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 324  
RESULT 5  
TGF2\_CHICK  
ID TGF2\_CHICK STANDARD; PRT; 412 AA.  
AC P30371;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
GN Name=TGFb2;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
CX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White leghorn; TISSUE=Blood;  
RX MEDLINE=92075163; PubMed=1683775;  
RA Burt D.W., Paton I.R.;  
RT "Molecular cloning and primary structure of the chicken transforming  
RT growth factor-beta 2 gene";  
RL DNA Cell Biol. 10:723-734(1991).  
CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2  
CC dependent T-cell growth.  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
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CC -----  
DR EMBL; X58071; CAA41101.1; -;  
DR EMBL; X59082; CAA41101.1; JOINED.  
DR EMBL; X59081; CAA41101.1; JOINED.  
DR EMBL; X59080; CAA41101.1; JOINED.  
DR PIR; A39489; A39489.

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DR HSP: P08112; 2TGI.
DR InterPro: IPR002400; GF cystknot.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR InterPro: IPR000911; TGF.TGFB.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR Pfam: PF00019; TGF.beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFb.BETA.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF.BETA.1; 1.
KW Glycoprotein; Growth factor; Mitogen; Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 300 Transforming growth factor beta 2.
FT CHAIN 301 412 By similarity.
FT DISULFID 307 316 By similarity.
FT DISULFID 315 378 By similarity.
FT DISULFID 344 409 By similarity.
FT DISULFID 348 411 By similarity.
FT DISULFID 377 377 Interchain (By similarity).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 240 240 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 412 AA; 47606 MW; 93E759BF1BD958DC CRC64;

Query Match 100.0%; Score 163; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQNCCLRLPLVDFKRDLG 29
DB 301 ALDAAVCFRNVQNCCLRLPLVDFKRDLG 329

RESULT 6
ID _TGF2_CERAE STANDARD; PRT; 414 AA.
AC P61811; P08112; Q15579; Q15581;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 2 precursor (TGF-beta 2)
DE (Glioblastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell
DE growth inhibitor) (Polyergin).
GN Names: TGFb2;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88124824; PubMed=3277172;
RA Hanks S., Armour R., Baldwin J.H., Maldonado F., Spiess J.,
RA Holley R.W.;
RT "Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin)
RT deduced from the nucleotide sequence of the cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 85:79-82(1988).
CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2
CC dependent T-cell growth.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC

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EMBL: J03585; AAA35358.1; -.
PIR: A34005; WPMKB2.
GO: GO:0005615; C:extracellular space; TAS.
GO: GO:0005160; F:transforming growth factor beta receptor bi...; TAS.
GO: GO:0008283; P:cell proliferation; TAS.
GO: GO:0007267; P:cell-cell signaling; TAS.
GO: GO:0007165; P:signal transduction; TAS.
InterPro: IPR002400; GF cystknot.
InterPro: IPR001839; TGFb.
InterPro: IPR001111; TGFb.N.
InterPro: IPR003911; TGF.TGFB.
Pfam: PF00688; TGFb.propeptide; 1.
Pfam: PF00019; TGF.beta; 1.
PRINTS: PR00438; GFCYSKNOT.
PRINTS: PR01423; TGFb.BETA.
ProDom: PD000357; TGFb; 1.
SMART: SM00204; TGFb; 1.
PROSITE: PS00250; TGF.BETA.1; 1.
KW Glycoprotein; Growth factor; Mitogen; Signal.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 302 By similarity.
FT CHAIN 303 414 Transforming growth factor beta 2.
FT DISULFID 309 318 By similarity.
FT DISULFID 317 380 By similarity.
FT DISULFID 346 411 By similarity.
FT DISULFID 350 413 By similarity.
FT DISULFID 379 379 Interchain (By similarity).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 414 AA; 47747 MW; 7D9D569E0F4A07D0 CRC64;

Query Match 100.0%; Score 163; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQNCCLRLPLVDFKRDLG 29
DB 303 ALDAAVCFRNVQNCCLRLPLVDFKRDLG 331

RESULT 7
ID _TGF2_HUMAN STANDARD; PRT; 414 AA.
AC P61812; P08112; Q15579; Q15581;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Transforming growth factor beta 2 precursor (TGF-beta 2)
DE (Glioblastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell
DE growth inhibitor) (Polyergin) (Cetermin).
GN Name: TGFb2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=88111555; PubMed=332813;
RA de Martin R., Haendler B., Hofer-Warbinek R., Gaugitsch H., Wrann M.,
RA Schluesener H., Seifert J.M., Bodmer S., Fontana A., Hofer E.;
RT "Complementary DNA for human glioblastoma-derived T cell suppressor
RT factor, a novel member of the transforming growth factor-beta gene
RT family."
RL EMBL J. 6:3673-3677(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=88166349; PubMed=3162414;
RA Madisen L., Webb N.R., Rose T.M., Marguardt H., Ikeda T.,
RA Twardzik D.R., Seyedin S., Purchio A.F.;
RT "Transforming growth factor-beta 2: cDNA cloning and sequence
RT analysis."
RL DNA 7:11-8(1988).

```

RN [3] SEQUENCE FROM N.A. (ISOFORM A), AND VARIANTS HIS-91 AND LEU-207.  
 RP MEDLINE=99090808; PubMed=2850146;  
 RX Webb N.R., Madisen L., Rose T.M., Purchio A.F.;  
 RA "Structural and sequence analysis of TGF-beta 2 cDNA clones predicts  
 RT two different precursor proteins produced by alternative mRNA  
 RL splicing.";  
 RL DNA 7:493-497(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A), AND VARIANTS HIS-91 AND LEU-207.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schackwitz W.S., Sherwood J.K., Witlak L.A., Nickerson D.A.;  
 RT "NIHNS-SNPs, environmental genome project, NIHNS E515478, Department  
 of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-115 FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=921110032; PubMed=1764261;  
 RA Noma T., Glick A.B., Geiser A.G., O'Reilly M.A., Miller J.,  
 RA Roberts A.B., Sporn M.B.;  
 RT "Molecular cloning and structure of the human transforming growth  
 factor-beta 2 gene promoter";  
 RL Growth Factors 4:247-255(1991).  
 RN [6]  
 RP SEQUENCE OF 303-414.  
 RX MEDLINE=87308213; PubMed=3476488;  
 RA Marquardt H., Lioubin M.N., Ikeda T.;  
 RT "Complete amino acid sequence of human transforming growth factor type  
 beta 2.";  
 RL J. Biol. Chem. 262:12127-12131(1987).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=92335881; PubMed=1631557;  
 RA Daopin S., Piez K.A., Ogawa Y., Davies D.R.;  
 RT "Crystal structure of transforming growth factor-beta 2: an unusual  
 fold for the superfamily.";  
 RL Science 257:369-373(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=92350287; PubMed=1641027;  
 RA Schlunegger M.P., Gruetter M.G.;  
 RT "An unusual feature revealed by the crystal structure at 2.2-A  
 resolution of human transforming growth factor-beta 2.";  
 RL Nature 358:430-434(1992).  
 RN [9]  
 RP VARIANT HIS-91.  
 RX MEDLINE=21419167; PubMed=11528528; DOI=10.1038/sj/gene/6363780;  
 RA Alansari A., Hajeer A.H., Bayat A., Eyre S., Carthy D., Ollier W.E.;  
 RT "Two novel polymorphisms in the human transforming growth factor beta  
 2 gene.";  
 RL Genes Immun. 2:295-296(2001).  
 CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2  
 dependent T-cell growth.  
 CC -!- SUBUNIT: Homodimer; disulfide-linked.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=A;  
 CC IsoId=P61812-1, P08112-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=P61812-2, P08112-2; Sequence=VSP\_006417;  
 CC -!- SIMILARITY: Belongs to the TGF-beta family.  
 CC  
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 CC -----

DR EMBL; Y00083; CAA68279.1; --  
 DR EMBL; M19154; AAA50404.1; --  
 DR EMBL; M19154; AAA50405.1; ALT\_SEQ.  
 DR EMBL; AY438979; AAR05442.1; --  
 DR EMBL; M87843; AAG61162.1; --  
 DR PIR; A29478; B31249.  
 DR PIR; S06216; A31249.  
 DR PDB; 1TFG; X-ray; --  
 DR PDB; 2TGI; X-ray; --  
 DR Genew; HGNC:11768; TGFb2.  
 DR MIM; 190220; --  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0005160; F:transforming growth factor beta receptor bi.; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR002400; GF\_cysknct.  
 DR InterPro; IPR001839; TGFb\_N.  
 DR InterPro; IPR001839; TGFb\_N.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR PRINTS; PR00438; GFCYSKNCT.  
 DR PRINTS; PR01423; TGFb2.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR 3D-structure; Alternative splicing; Direct protein sequencing;  
 KW Glycoprotein; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 19 Potential.  
 FT PROPEP 20 302 Transforming growth factor beta 2.  
 FT CHAIN 303 414  
 FT DISULFID 309 318  
 FT DISULFID 317 380  
 FT DISULFID 346 411  
 FT DISULFID 350 413  
 FT DISULFID 379 379  
 FT CARBOHYD 72 72  
 FT CARBOHYD 140 140  
 FT CARBOHYD 241 241  
 FT VARSPLIC 116 116  
 FT  
 FT VARIANT 91 91  
 FT VARIANT 207 207  
 FT  
 FT CONFLICT 32 32  
 FT HELIX 306 309  
 FT TURN 310 311  
 FT STRAND 316 316  
 FT STRAND 318 320  
 FT STRAND 323 325  
 FT HELIX 326 330  
 FT TURN 333 334  
 FT STRAND 335 337  
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 FT TURN 352 353  
 FT STRAND 356 356  
 FT HELIX 359 370  
 FT STRAND 372 374  
 FT HELIX 380 382  
 FT STRAND 385 394  
 FT TURN 395 396  
 FT STRAND 397 408  
 FT STRAND 411 414  
 SQ SEQUENCE 414 AA; 47747 MW; 7D9D569E0F4A07D0 CRC64;  
 Query Match 100.0%; Score 163; DB 1; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 15e-15;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKDLG 29  
 |||||  
 DB 303 ALDAAACFRNVQDNCCLRLPLYIDFKDLG 331

## RESULT 8

TF2 MOUSE STANDARD; PRT; 414 AA.  
 AC P27050;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 03-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
 GN Name=Tgfb2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90014832; PubMed=2797004;  
 RA Miller D.A., Lee A., Pelton R.W., Chen E.Y., Moses H.L., Derynck R.;  
 RT "Murine transforming growth factor-beta 2 cDNA sequence and expression  
 in adult tissues and embryos";  
 RL Mol. Endocrinol. 3:1108-1114(1989).  
 CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2  
 dependent T-cell growth.  
 CC -!- SUBUNIT: Homodimer; disulfide-linked.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the TGF-beta family.  
 CC  
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 CC  
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DR EMBL; X57413; CAA0672.1; -;  
 DR PIR; A40148; WFM5B2.  
 DR HSP; P08112; 2TGI.  
 DR MGD; MGI:98726; Tgfb2.  
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.  
 DR InterPro; IPR002400; GFCysknot.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR PRINTS; PR01423; TGFbeta.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR GlycoProtein; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 19 Potential.  
 FT PROPEP 20 302 Transforming growth factor beta 2.  
 FT CHAIN 303 414 By similarity.  
 FT DISULFID 309 414 By similarity.  
 FT DISULFID 317 380 By similarity.  
 FT DISULFID 346 411 By similarity.  
 FT DISULFID 350 413 By similarity.  
 FT DISULFID 379 379 Interchain (By similarity).  
 FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 414 AA; 47601 MW; 449BC6FA22087FB6 CRC64;

Query Match 100.0%; Score 163; DB 1; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKDLG 29  
 |||||  
 DB 303 ALDAAACFRNVQDNCCLRLPLYIDFKDLG 331

## RESULT 9

Q91VP5 PRELIMINARY; PRT; 414 AA.  
 AC Q91VP5;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Transforming growth factor, beta 2.  
 GN Name=Tgfb2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 EX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiruki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalusz J., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the TGF-beta family.  
 DR EMBL; BC011170; AA01170.1; -;  
 DR HSP; P08112; 2TGI.  
 DR MGD; MGI:98726; Tgfb2.  
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.  
 DR InterPro; IPR002400; GFCysknot.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR003940; TGFb2.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR001111; TGFb\_N.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR PRINTS; PR01423; TGFbeta.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor.  
 SQ SEQUENCE 414 AA; 47588 MW; DB37A7C38881F286 CRC64;

Query Match 100.0%; Score 163; DB 2; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLIDFKRDLG 29  
DB 303 ALDAAFCFRNVQDNCCLRLPLIDFKRDLG 331

RESULT 10  
TGF2\_PIG STANDARD; PRT; 435 AA.  
AC P09858;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
GN Name=TGFbeta2;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE OF 2-435 FROM N.A.  
RC TISSUE=Lung;  
RA Zhou Y.;  
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 303-345.  
RX MEDLINE=87102890; PubMed=2879635;  
RA Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,  
RA Lucas R., Massague J.;  
RT "The transforming growth factor-beta system, a complex pattern of  
RT cross-reactive ligands and receptors.";  
RL Cell 48:409-415(1987).  
CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the TGF-beta family.

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CC -----  
DR EMBL; L08375; AAB03850.1; -.  
DR HSSP; P08112; 2TGI.  
DR InterPro; IPR002400; GF\_cysknot.  
DR InterPro; IPR001839; TGFb\_N.  
DR InterPro; IPR001111; TGFb\_N.  
DR InterPro; IPR003911; TGF\_TGFB.  
DR Pfam; PF00688; TGFb\_propeptide; 1.  
DR Pfam; PF00019; TGF\_beta; 1.  
DR PRINTS; PR00438; GFCYSKNOT.  
DR PRINTS; PR01423; TGFbeta.  
DR ProDom; PD000357; TGFb; 1.  
DR SMART; SMO0204; TGFb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
KW Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;  
Signal.  
FT PROPEP 1 19 Potential.  
FT CHAIN 20 302 Transforming growth factor beta 2.  
FT DISULFID 303 435 By similarity.  
FT DISULFID 309 318 By similarity.  
FT DISULFID 317 380 By similarity.  
FT DISULFID 346 411 By similarity.  
FT DISULFID 350 413 By similarity.  
FT DISULFID 379 379 Interchain (By similarity).  
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 435 AA; 49922 MW; 438282E288B32322 CRC64;

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QY 1 ALDAAFCFRNVQDNCCLRLPLIDFKRDLG 29  
DB 303 ALDAAFCFRNVQDNCCLRLPLIDFKRDLG 331

RESULT 11  
TGF2\_RAT STANDARD; PRT; 442 AA.  
AC Q07257; Q63574; Q9QW26; Q9R281; Q9R298; Q9R2B8; Q9WUQ8;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
GN Name=Tgfb2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS TGF-BETA2A AND TGF-BETA2B).  
RC STRAIN=Wistar; TISSUE=Muscle;  
RA Koishi K., Dalzell K.G.B., McLennan I.S.;  
RT "Structure and expression of TGF-beta 2 messages in the rat muscle.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM TGF-BETA2A).  
RC STRAIN=Wistar;  
RA Konrad L., Albrecht M., Amueller G.;  
RT "The rat TGF-beta2 gene: sequence analysis and expression pattern in  
RT the rat testis.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM TGF-BETA2A).  
RA Plisov S.Y., Ivanov S.V., Plisova T.M., Lerman M., Perantoni A.O.;  
RT "Rat transforming growth factor-beta2, complete coding sequence.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 278-348 FROM N.A.  
RX MEDLINE=93286190; PubMed=9509457;  
RA McKinnon R.D., Piras G., Ida J., Dubois-Daig M.;  
RT "A role for TGF-beta in oligodendrocyte differentiation.";  
RL J. Cell Biol. 121:1397-1407(1993).  
RN [5]  
RP SEQUENCE OF 366-441 FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Heart;  
RX MEDLINE=93253033; PubMed=8486763;  
RA Nishida M., Springhorn J.P., Kelly R.A., Smith T.W.;  
RT "Cell-cell signaling between adult rat ventricular myocytes and  
RT cardiac microvascular endothelial cells in heterotypic primary  
RT culture.";  
RL J. Clin. Invest. 91:1934-1941(1993).  
CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2  
CC -!- dependent T-cell growth.  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=TGF-beta2B;  
CC IsoId=Q07257-1; Sequence=Displayed;  
CC Name=TGF-beta2A;  
CC IsoId=Q07257-2; Sequence=VSP\_006418, VSP\_006419;  
CC -!- SIMILARITY: Belongs to the TGF-beta family.

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CC DR EMBL; AF153012; AAD34159.1; -.
CC DR EMBL; AF132718; CAB42003.1; -.
CC DR EMBL; AF153013; AAD34160.1; -.
CC DR EMBL; AF135598; AAD24484.1; -.
CC DR EMBL; X71904; CAA50723.1; -.
CC DR EMBL; M96643; AAA88514.1; ALT_SEQ.
CC DR PIR; A40699; A40699.
CC DR HSP; P08112; TGFb2.
CC DR RGD; 70491; TGFb2.
CC DR InterPro; IPR002400; GF_cysknot.
CC DR InterPro; IPR001839; TGFb.
CC DR InterPro; IPR001111; TGFb N.
CC DR InterPro; IPR003911; TGF_TGFb.
CC DR Pfam; PF00688; TGFb_propeptide; 1.
CC DR Pfam; PF00019; TGF_beta; 1.
CC DR PRINTS; PR01423; GFCYSKNOT.
CC DR PRINTS; PR01423; TGFbBETA.
CC DR PRODOM; PD000357; TGFb; 1.
CC DR SMART; SMO0204; TGFb; 1.
CC DR PROSITE; PS00250; TGF_BETA_1; 1.
CC DR ALTERNATIVE SPLICING; Glycoprotein; Growth factor; Mitogen; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 330 Transforming growth factor beta 2.
FT CHAIN 331 442 By similarity.
FT DISULFID 337 346 By similarity.
FT DISULFID 345 348 By similarity.
FT DISULFID 374 439 By similarity.
FT DISULFID 378 441 By similarity.
FT DISULFID 407 407 Interchain (by similarity).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 269 269 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 116 143 Missing (in isoform TGF-beta2A).
FT VARSPLIC 144 144 D->N (in isoform TGF-beta2A).
FT CONFLICT 99 99 Y->C (in Ref. 2).
FT CONFLICT 310 310 L->P (in Ref. 3).
FT CONFLICT 343 343 D->H (in Ref. 2 and 4).
SQ SEQUENCE 442 AA; 50533 MW; 69C81A19CE06C253 CRC64;

Query Match 100.0%; Score 163; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFNRVQDNCCLRPYIDFKRDLG 29
Db 331 ALDAAYCFNRVQDNCCLRPYIDFKRDLG 359

RESULT 12
Q6T7C3 PRELIMINARY; PRT; 442 AA.
AC Q6T7C3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transforming growth factor-beta 2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Man X.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AY429466; AAR06973.1; -.
DR InterPro; IPR002400; GF_cysknot.

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DR InterPro; IPR001839; TGFb.
DR InterPro; IPR003940; TGFb2.
DR InterPro; IPR001111; TGFb N.
DR InterPro; IPR003911; TGF_TGFb.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbBETA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 442 AA; 50533 MW; AFB64148E893C93E CRC64;

Query Match 100.0%; Score 163; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFNRVQDNCCLRPYIDFKRDLG 29
Db 331 ALDAAYCFNRVQDNCCLRPYIDFKRDLG 359

RESULT 13
AAR06973 PRELIMINARY; PRT; 442 AA.
AC AAR06973
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Transforming growth factor-beta 2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Man X.;
RL "Cloning of rabbit transforming growth factor beta 2.";
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429466; AAR06973.1; -.
SQ SEQUENCE 442 AA; 50533 MW; AFB64148E893C93E CRC64;

Query Match 100.0%; Score 163; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFNRVQDNCCLRPYIDFKRDLG 29
Db 331 ALDAAYCFNRVQDNCCLRPYIDFKRDLG 359

RESULT 14
TGF2_XENLA STANDARD; PRT; 413 AA.
AC TGF2_XENLA
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 2 precursor (TGF-beta 2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90245678; PubMed=2336403;
RA Rebert M.L., Bhatia-Dey N., David I.B.;
RT "The sequence of TGF-beta 2 from Xenopus laevis.";
RL Nucleic Acids Res. 18:2185-2185(1990).

```



CC -!- FUNCTION: TGF-beta 2 has suppressive effects on interleukin-2  
CC dependent T-cell growth.  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
CC -----  
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CC -----  
CC EMBL; X51817; CAA36116.1; -  
CC EMBL; X51817; CAA36117.1; ALT\_INIT.  
CC PIR; S09510; WFLB2.  
CC HSSP; P08112; 2TGI.  
CC InterPro; IPR002400; GF\_cys\_knot.  
CC InterPro; IPR001839; TGFb.  
CC InterPro; IPR001111; TGFb\_N.  
CC InterPro; IPR003911; TGF\_TGFB.  
CC Pfam; PF00688; TGFb\_propeptide; 1.  
CC Pfam; PF00019; TGF\_beta; 1.  
CC PRINTS; PR00438; GFCYSKNOT.  
CC PRINTS; PR01423; TGFbETA.  
CC ProDom; PD000357; TGFb; 1.  
CC SMART; SM00204; TGFb; 1.  
CC PROSITE; PS00250; TGF\_BETA\_1; 1.  
CC GlycoProtein; Growth factor; Mitogen; Signal.  
CC FT SIGNAL 1 19 Potential.  
CC FT PROPEP 20 301 Transforming growth factor beta 2.  
CC FT CHAIN 302 413 By similarity.  
CC FT DISULFID 308 317 By similarity.  
CC FT DISULFID 316 379 By similarity.  
CC FT DISULFID 345 410 By similarity.  
CC FT DISULFID 349 412 By similarity.  
CC FT DISULFID 378 378 Interchain (By similarity).  
CC FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).  
CC SQ SEQUENCE 413 AA; 47639 MW; 6127715B38734010 CRC64;  
Query Match 98.2%; Score 160; DB 1; Length 413;  
Best Local Similarity 96.6%; Pred. No. 4.2e-15;  
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 29  
DB 302 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 330  
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Q98854 PRELIMINARY; PRT; 361 AA.  
AC Q98854;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transforming growth factor beta 2 (TGF-beta 2) (Fragment).  
GN Name=TGFb2;  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA MEDLINE=97354301; PubMed=9210595;  
RX Sumathy K., Desai K.V., Kondaiah P.;  
RT "Isolation of transforming growth factor-beta2 cDNA from a fish,  
Cyprinus carpio by RT-PCR.";

RL Gene 191:103-107(1997).  
CC -!- FUNCTION: Has suppressive effects on interleukin-2 dependent T-  
CC cell growth.  
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
CC EMBL; U66874; AAB62983.1; -  
CC HSSP; P08112; 2TGI.  
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CC DR GO; GO:0005160; F:Transforming growth factor beta receptor bi.; IEA.  
CC DR GO; GO:0016049; P:Cell growth; IEA.  
CC DR GO; GO:0008283; P:Cell proliferation; IEA.  
CC DR GO; GO:0000074; P:Regulation of cell cycle; IEA.  
CC DR InterPro; IPR001839; TGFb.  
CC DR InterPro; IPR003940; TGFb2.  
CC DR InterPro; IPR001111; TGFb\_N.  
CC DR InterPro; IPR003911; TGF\_TGFB.  
CC Pfam; PF00688; TGFb\_propeptide; 1.  
CC Pfam; PF00019; TGF\_beta; 1.  
CC PRINTS; PR01423; TGFbETA.  
CC PRINTS; PR01425; TGFbETA2.  
CC ProDom; PD000357; TGFb; 1.  
CC SMART; SM00204; TGFb; 1.  
CC PROSITE; PS00250; TGF\_BETA\_1; 1.  
CC GlycoProtein; Growth factor; Mitogen.  
CC FT NON\_TER 1 1  
CC FT PROPEP <1 257 TRANSFORMING GROWTH FACTOR BETA 2.  
CC FT CHAIN 258 361 BY SIMILARITY.  
CC FT DISULFID 264 273 BY SIMILARITY.  
CC FT DISULFID 272 335 INTERCHAIN (BY SIMILARITY).  
CC FT DISULFID 334 334 N-LINKED (GLCNAC...) (POTENTIAL).  
CC FT CARBOHYD 30 30 N-LINKED (GLCNAC...) (POTENTIAL).  
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC...) (POTENTIAL).  
CC FT CARBOHYD 199 199  
CC FT NON\_TER 361 361  
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DB 258 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 286  
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Job time : 191 secs

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OM protein - protein search, using sw model

Run on: October 31, 2004, 14:17:05 ; Search time 37 Seconds  
(without alignments)  
254.115 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAFCFRNVQNCCLRLPLIDFKRDGLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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17: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	100.0	29	9	US-09-822-873-1
2	163	100.0	29	14	US-10-240-421-1
3	163	100.0	60	10	US-09-791-301-123
4	163	100.0	70	9	US-09-848-664-10
5	163	100.0	112	9	US-09-813-271B-4
6	163	100.0	112	9	US-09-813-271B-10
7	163	100.0	112	14	US-10-366-345-55
8	163	100.0	113	9	US-09-813-398-14
9	163	100.0	114	9	US-09-389-705-24
10	163	100.0	114	9	US-09-813-459-23
11	163	100.0	114	13	US-10-115-406-22
12	163	100.0	114	14	US-10-154-333-24
13	163	100.0	114	16	US-10-704-223-22

14	163	100.0	115	9	US-09-859-211-48	Sequence 48, Appl
15	163	100.0	115	9	US-09-880-708-26	Sequence 26, Appl
16	163	100.0	115	10	US-09-872-856-48	Sequence 48, Appl
17	163	100.0	115	14	US-10-335-483-30	Sequence 30, Appl
18	163	100.0	115	15	US-10-463-973-48	Sequence 48, Appl
19	163	100.0	115	15	US-10-693-536-20	Sequence 20, Appl
20	163	100.0	115	16	US-10-758-210-20	Sequence 68, Appl
21	163	100.0	387	15	US-10-080-334-68	Sequence 30, Appl
22	163	100.0	412	10	US-09-214-592-30	Sequence 24, Appl
23	163	100.0	414	9	US-09-756-283A-24	Sequence 18, Appl
24	163	100.0	414	10	US-09-214-592-18	Sequence 21, Appl
25	163	100.0	414	10	US-09-214-592-21	Sequence 204, Appl
26	163	100.0	414	15	US-10-080-334-204	Sequence 207, Appl
27	163	100.0	414	15	US-10-058-270A-116	Sequence 116, Appl
28	163	100.0	414	15	US-10-080-334-206	Sequence 205, Appl
29	163	100.0	434	15	US-10-080-334-205	Sequence 47, Appl
30	163	100.0	435	15	US-10-366-345-47	Sequence 203, Appl
31	163	100.0	442	14	US-10-366-345-47	Sequence 124, Appl
32	163	100.0	442	15	US-10-080-334-203	Sequence 11, Appl
33	133	81.6	60	10	US-09-791-301-124	Sequence 6, Appl
34	133	81.6	70	9	US-09-848-664-11	Sequence 12, Appl
35	133	81.6	112	9	US-09-813-271B-6	Sequence 56, Appl
36	133	81.6	112	9	US-09-813-271B-12	Sequence 15, Appl
37	133	81.6	112	14	US-10-366-345-56	Sequence 25, Appl
38	133	81.6	113	9	US-09-813-398-15	Sequence 24, Appl
39	133	81.6	114	9	US-09-389-705-25	Sequence 23, Appl
40	133	81.6	114	13	US-10-115-406-23	Sequence 25, Appl
41	133	81.6	114	14	US-10-154-333-25	Sequence 23, Appl
42	133	81.6	114	16	US-10-704-223-23	Sequence 49, Appl
43	133	81.6	114	16	US-10-704-223-23	Sequence 27, Appl
44	133	81.6	115	9	US-09-859-211-49	
45	133	81.6	115	9	US-09-880-708-27	

#### ALIGNMENTS

#### RESULT 1

US-09-822-873-1  
; Sequence 1, Application US/09822873  
; Patent No. US20020160012A1  
; GENERAL INFORMATION:  
; APPLICANT: KAASTRUP, Peter  
; TITLE OF INVENTION: VACCINE CHIP TECHNOLOGY EXPLOITING IMMUNO-STIMULATING FRAGMENT OF  
; FILE REFERENCE: KAASTRUP-1A  
; CURRENT APPLICATION NUMBER: US/09/822,873  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/246,973  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: DK PA2000 00540  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; TYPE: PRT  
; LENGTH: 29  
; ORGANISM: Homo sapiens  
US-09-822-873-1

Query Match 100.0%; Score 163; DB 9; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.8e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQNCCLRLPLIDFKRDGLG 29  
Db 1 ALDAAFCFRNVQNCCLRLPLIDFKRDGLG 29

#### RESULT 2

US-10-240-421-1  
; Sequence 1, Application US/10240421  
; Publication No. US20030190322A1

```

; GENERAL INFORMATION:
; APPLICANT: KASTRUP, Peter
; TITLE OF INVENTION: IMMUNOSTIMULATING PROPERTIES OF A FRAGMENT OF TGF-BETA
; FILE REFERENCE: KASTRUP-2
; CURRENT APPLICATION NUMBER: US/10/240,421
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-421-1

Query Match          100.0%; Score 163; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLYIDFKRDLG 29
Db 1 ALDAAYCFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 3
US-09-791-301-123
; Sequence 123, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR FILING DATE: 09/046,247
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver..2.0
; SEQ ID NO 123
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-791-301-123

Query Match          100.0%; Score 163; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.8e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLYIDFKRDLG 29
Db 1 ALDAAYCFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 4
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```

US-09-848-664-110
; Sequence 10, Application US/09848664
; Patent No. US20020146414A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Elbert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/298,084
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664-110

Query Match          100.0%; Score 163; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLYIDFKRDLG 29
Db 1 ALDAAYCFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 5
US-09-813-271B-4
; Sequence 4, Application US/09813271B
; Patent No. US20020115834A1
; GENERAL INFORMATION:
; APPLICANT: (A) Nico Cerletti
; TITLE OF INVENTION: New process for the production of
; biologically active protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020115834A1
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,271B
; FILING DATE: 20-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02719
; FILING DATE: 12-Jul-95
; APPLICATION NUMBER: EPO 94810439.3
; FILING DATE: 25-Jul-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Hessa J..
; REGISTRATION NUMBER: 22640
; REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6940
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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## RESULT 7

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/389,705  
FILING DATE: 03-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/153,733  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
IMMEDIATE SOURCE:  
CLONE: TGF-beta 2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-389-705-24

Query Match 100.0%; Score 163; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 3 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 31

RESULT 10  
US-09-813-459-23  
Sequence 23, Application US/09813459  
Patent No. US20020107369A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
Cunningham, No. US20020107369Aleen  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,459  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/624,635  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3054  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-813-459-23

Query Match 100.0%; Score 163; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 3 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 31

RESULT 11  
US-10-115-406-22  
Sequence 22, Application US/10115406  
Publication No. US20020127612A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
Lee, Se-Jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
FILE REFERENCE: JHUI190-3  
CURRENT APPLICATION NUMBER: US/10/115,406  
CURRENT FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: 09/301,520  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: US 09/172,062  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/491,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: PCT/US94/00685  
PRIOR FILING DATE: 1994-01-12  
PRIOR APPLICATION NUMBER: US 08/003,303  
PRIOR FILING DATE: 1993-01-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 22  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-406-22

Query Match 100.0%; Score 163; DB 13; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 3 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 31

RESULT 12  
US-10-154-333-24  
Sequence 24, Application US/10154333  
Publication No. US20030109684A1  
GENERAL INFORMATION:  
APPLICANT: JOHNS HOPKINS UNIVERSITY  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 21-May-2002  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION NUMBER: US/10/154,333  
PRIORITY APPLICATION DATA:  
FILING DATE: 03-Sep-1999  
APPLICATION NUMBER: 09/153,733  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta 2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-154-333-24  
Query Match 100.0%; Score 163; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAACFRNVQDNCCLRLPLIDFKRDLG 29  
Db 3 ALDAAACFRNVQDNCCLRLPLIDFKRDLG 31  
RESULT 13  
US-10-704-223-22  
Sequence 22, Application US/10704223  
Publication No. US20040152143A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
APPLICANT: Lee, Se-jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
FILE REFERENCE: JH01190-7  
CURRENT APPLICATION NUMBER: US/10/704,223  
CURRENT FILING DATE: 2003-11-07  
PRIOR APPLICATION NUMBER: US 10/115,406  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: US 09/301,520  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: US 09/172,062  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/491,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: PCT/US94/00685  
PRIOR FILING DATE: 1994-01-12  
PRIOR APPLICATION NUMBER: US 08/003,303

PRIOR FILING DATE: 1993-01-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-704-223-22  
Query Match 100.0%; Score 163; DB 16; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAACFRNVQDNCCLRLPLIDFKRDLG 29  
Db 3 ALDAAACFRNVQDNCCLRLPLIDFKRDLG 31  
RESULT 14  
US-09-859-211-48  
Sequence 48, Application US/09859211  
Patent No. US20020157125A1  
GENERAL INFORMATION:  
APPLICANT: McPherson, Alexandra C.  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
FILE REFERENCE: 07265/144001  
CURRENT APPLICATION NUMBER: US/09/859,211  
CURRENT FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: 09/019,070  
PRIOR FILING DATE: 1998-02-05  
PRIOR APPLICATION NUMBER: 08/862,445  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 08/847,910  
PRIOR FILING DATE: 1997-04-28  
PRIOR APPLICATION NUMBER: 08/795,071  
PRIOR FILING DATE: 1997-02-05  
PRIOR APPLICATION NUMBER: 08/525,596  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: PCT/US94/03019  
PRIOR FILING DATE: 1994-03-18  
PRIOR APPLICATION NUMBER: 08/033,923  
PRIOR FILING DATE: 1993-03-19  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 48  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-859-211-48  
Query Match 100.0%; Score 163; DB 9; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAACFRNVQDNCCLRLPLIDFKRDLG 29  
Db 4 ALDAAACFRNVQDNCCLRLPLIDFKRDLG 32  
RESULT 15  
US-09-880-708-26  
Sequence 26, Application US/09880708  
Patent No. US20020165361A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-jin  
APPLICANT: Huynh, Thanh  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego

STATE: CA  
COUNTRY: USA  
ZIP: 92121-2189  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/880,708  
FILING DATE: 12-Jun-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/145,060  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/003,144  
FILING DATE: 12-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lisa A. Hailer, Ph.D.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/057002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858/677-1456  
TELEFAX: 619/677-1456  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-880-708-26  
Query Match 100.0%; Score 163; DB 9; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALDAAACFRNVQDNCCLRPYIDFKRDLG 29  
Db 4 ALDAAACFRNVQDNCCLRPYIDFKRDLG 32  
RESULT 16  
US-09-872-856-48  
Sequence 48, Application US/09872856  
Publication No. US20030074680A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
APPLICANT: McPherson, Alexandra  
TITLE OF INVENTION: Growth Differentiation Factor-8  
FILE REFERENCE: JHU1120-17  
CURRENT APPLICATION NUMBER: US/09/872,856  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: US 09/124,180  
PRIOR FILING DATE: 1998-07-28  
PRIOR APPLICATION NUMBER: US 09/019,070  
PRIOR FILING DATE: 1998-02-05  
PRIOR APPLICATION NUMBER: US 08/862,445  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: US 08/847,910  
PRIOR FILING DATE: 1997-04-28  
PRIOR APPLICATION NUMBER: US 08/795,071  
PRIOR FILING DATE: 1997-02-05  
PRIOR APPLICATION NUMBER: US 08/525,596  
PRIOR FILING DATE: 1995-10-25  
PRIOR APPLICATION NUMBER: PCT/US 94/03019  
PRIOR FILING DATE: 1994-03-18  
PRIOR APPLICATION NUMBER: US 08/033,923  
PRIOR FILING DATE: 1993-03-19  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 48  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-872-856-48  
Query Match 100.0%; Score 163; DB 10; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALDAAACFRNVQDNCCLRPYIDFKRDLG 29  
Db 4 ALDAAACFRNVQDNCCLRPYIDFKRDLG 32  
RESULT 17  
US-10-335-483-30  
Sequence 30, Application US/10335483  
Publication No. US20030120058A1  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
Lee, Se-Jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/335,483  
FILING DATE: 31-Dec-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: PCT/US94/07762  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D, John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 07265/075001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-10-335-483-30  
Query Match 100.0%; Score 163; DB 14; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALDAAACFRNVQDNCCLRPYIDFKRDLG 29





Db 4 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 32

## RESULT 21

US-10-080-334-68

; Sequence 68, Application US/10080334  
; Publication No. US2004002584A1

## GENERAL INFORMATION:

; APPLICANT: Pena, Carol E. A.  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Li, Li  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc L  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Gangolli, Baha A  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Baumgarther, Jason C.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Zerhusen, Bryan D

; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

; FILE REFERENCE: 21402-275

; CURRENT APPLICATION NUMBER: US/10/080,334  
; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 60/270,523

; PRIOR FILING DATE: 2001-02-21

; PRIOR APPLICATION NUMBER: 60/322,712

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: 60/311,980

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 60/330,307

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/278,796

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: 60/281,521

; PRIOR FILING DATE: 2001-04-04

; PRIOR APPLICATION NUMBER: 60/276,677

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/311,595

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/270,220

; PRIOR FILING DATE: 2001-02-21

; PRIOR APPLICATION NUMBER: 60/274,295

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/318,526

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/286,548

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: 60/291,765

; PRIOR FILING DATE: 2001-05-17

; PRIOR APPLICATION NUMBER: 60/270,797

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/276,400

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/270,810

; PRIOR FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 388

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 68

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-080-334-68

Query Match 100.0%; Score 163; DB 15; Length 387;

Best Local Similarity 100.0%; Pred. No. 2.4e-14;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 29

Db 276 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 304

## RESULT 22

US-09-214-592-30

; Sequence 30, Application US/0924592A

; Publication No. US20030027218A1

## GENERAL INFORMATION:

; APPLICANT: Yamasaki, CMotoo

; APPLICANT: Shibata, Ckenji

; APPLICANT: Sato, Cyasufumi

; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD

; FILE REFERENCE: 11060

; CURRENT APPLICATION NUMBER: US/09/214,592A

; CURRENT FILING DATE: 1999-01-18

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE:

; SEQ ID NO 30

; LENGTH: 412

; TYPE: PRT

; ORGANISM: chicken

US-09-214-592-30

Query Match 100.0%; Score 163; DB 10; Length 412;

Best Local Similarity 100.0%; Pred. No. 2.5e-14;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 29

Db 301 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 329

## RESULT 23

US-09-756-283A-24

; Sequence 24, Application US/09756283A

; Patent No. US20020151478A1

## GENERAL INFORMATION:

; APPLICANT: Chernajovsky, Yuti

; APPLICANT: Dreja, Hanna Stina

; APPLICANT: Adams, Gillian

; TITLE OF INVENTION: Latent Fusion Protein

; FILE REFERENCE: 0623.1000000

; CURRENT APPLICATION NUMBER: US/09/756,283A

; CURRENT FILING DATE: 2001-01-09

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 24

; LENGTH: 414

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-756-283A-24

Query Match 100.0%; Score 163; DB 9; Length 414;

Best Local Similarity 100.0%; Pred. No. 2.5e-14;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 29

Db 303 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 331

## RESULT 24

US-09-214-592-18

; Sequence 18, Application US/09214592A

```

; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Cmoroo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Cvasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 18
; LENGTH: 414
; TYPE: PRT
; ORGANISM: human
US-09-214-592-18

Query Match      100.0%; Score 163; DB 10; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALDAAAYCFRNVQDNCCLRPPLYIDFKRDLG 29
Db      303 ALDAAAYCFRNVQDNCCLRPPLYIDFKRDLG 331

RESULT 25
US-09-214-592-21
; Sequence 21, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Cmoroo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Cvasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 21
; LENGTH: 414
; TYPE: PRT
; ORGANISM: murine
US-09-214-592-21

Query Match      100.0%; Score 163; DB 10; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALDAAAYCFRNVQDNCCLRPPLYIDFKRDLG 29
Db      303 ALDAAAYCFRNVQDNCCLRPPLYIDFKRDLG 331

RESULT 26
US-10-080-334-204
; Sequence 204, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kexuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J

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; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zernhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-204

Query Match      100.0%; Score 163; DB 15; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALDAAAYCFRNVQDNCCLRPPLYIDFKRDLG 29
Db      303 ALDAAAYCFRNVQDNCCLRPPLYIDFKRDLG 331

RESULT 27
US-10-080-334-207
; Sequence 207, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li

```

APPLICANT: Shenoy, Suresh G  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Gusev, Vladimir Y  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Patturajan, Meera  
APPLICANT: Gangolli, Esha A  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Liu, Xiaohong  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spaderna, Steven K  
APPLICANT: Zerhusen, Bryan D  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
TITLE OF INVENTION: Using the Same  
FILE REFERENCE: 21402-275  
CURRENT APPLICATION NUMBER: US/10/080,334  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/270,523  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/322,712  
PRIOR FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: 60/311,980  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/330,307  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: 60/278,796  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/281,521  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/276,677  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/311,595  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/270,220  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/274,295  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/318,526  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 60/286,548  
PRIOR FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/291,765  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: 60/270,797  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/276,400  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/270,810  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 388  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 207  
LENGTH: 414  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-080-334-207

Query Match 100.0%; Score 163; DB 15; Length 414;  
Best Local Similarity 100.0%; Pred. No. 2.5e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 29  
Db 303 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 331

RESULT 28  
US-10-058-270A-116  
Sequence 116, Application US/10058270A  
Publication No. US20040029114A1  
GENERAL INFORMATION:  
APPLICANT: Mack, David H.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Afar, Daniel  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer  
FILE REFERENCE: 018501-005210US  
CURRENT APPLICATION NUMBER: US/10/058,270A  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: US 60/263,965  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/265,928  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: US 09/829,472  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: US 60/282,698  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: US 60/288,590  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/294,443  
PRIOR FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 116  
LENGTH: 414  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-058-270A-116

Query Match 100.0%; Score 163; DB 15; Length 414;  
Best Local Similarity 100.0%; Pred. No. 2.5e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 29  
Db 303 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 331

RESULT 29  
US-10-080-334-206  
Sequence 206, Application US/10080334  
Publication No. US20040002584A1  
GENERAL INFORMATION:  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Li, Li  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Gusev, Vladimir Y  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Patturajan, Meera  
APPLICANT: Gangolli, Esha A  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Liu, Xiaohong  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spaderna, Steven K  
APPLICANT: Zerhusen, Bryan D  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
TITLE OF INVENTION: Using the Same  
FILE REFERENCE: 21402-275

APPLICANT: Liu, Xiaohong  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spaderna, Steven K  
APPLICANT: Zetser, Bryan D  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
FILE REFERENCE: 21402-275  
CURRENT APPLICATION NUMBER: US/10/080,334  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/270,523  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/322,712  
PRIOR FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: 60/311,980  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/330,307  
PRIOR FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 60/278,796  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/281,521  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/276,677  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/311,595  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/270,220  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/274,295  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/318,526  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 60/286,548  
PRIOR FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/291,765  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: 60/270,797  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/276,400  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/270,810  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 206  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-080-334-206

Query Match 100.0%; Score 163; DB 15; Length 434;  
Best Local Similarity 100.0%; Pred. No. 2.7e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRLPLYIDFKRDLG 29  
|||||  
Db 302 ALDAAYCFRNVDNCCLRLPLYIDFKRDLG 330

RESULT 30  
US-10-080-334-205  
Sequence 205, Application US/10080334  
Publication No. US20040002584A1  
GENERAL INFORMATION:  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Shimkets, Richard A  
APPLICANT: Li, Li  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Guo, Xiaojia  
APPLICANT: Gusev, Vladimir Y  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Patturajan, Meera  
APPLICANT: Gangolli, Esha A  
APPLICANT: Padigaru, Muralidhara

APPLICANT: Liu, Xiaohong  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spaderna, Steven K  
APPLICANT: Zetser, Bryan D  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
FILE REFERENCE: 21402-275  
CURRENT APPLICATION NUMBER: US/10/080,334  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/270,523  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/322,712  
PRIOR FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: 60/311,980  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/330,307  
PRIOR FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 60/278,796  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/281,521  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/276,677  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/311,595  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/270,220  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/274,295  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/318,526  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 60/286,548  
PRIOR FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/291,765  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: 60/270,797  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/276,400  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/270,810  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 205  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Sus scrofa  
US-10-080-334-205

Query Match 100.0%; Score 163; DB 15; Length 435;  
Best Local Similarity 100.0%; Pred. No. 2.7e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRLPLYIDFKRDLG 29  
|||||  
Db 303 ALDAAYCFRNVDNCCLRLPLYIDFKRDLG 331

RESULT 31  
US-10-366-345-47  
Sequence 47, Application US/10366345  
Publication No. US20030224501A1  
GENERAL INFORMATION:  
APPLICANT: Young, et al.  
TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and  
FILE REFERENCE: PT189  
CURRENT APPLICATION NUMBER: US/10/366,345  
CURRENT FILING DATE: 2003-02-14  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47

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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-345-47

Query Match      100.0%; Score 163; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29
Db      331 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 359

RESULT 32
US-10-080-334-203
; Sequence 203, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Liu, Xiachong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zernhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
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; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-203

Query Match      100.0%; Score 163; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29
Db      331 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 359

Search completed: October 31, 2004, 14:29:07
Job time : 37 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 08:31:14 ; Search time 58 Seconds  
(without alignments)  
287.687 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 28853

Minimum DB seq length: 0

Maximum DB seq length: 29

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	36.2	20	2	Q6UQN2	Q6uqn2 anomalospiz
2	59	36.2	20	2	Q6UQN3	Q6uqn3 vidua orien
3	59	36.2	20	2	Q6UQN4	Q6uqn4 vidua parad
4	59	36.2	20	2	Q6UQN5	Q6uqn5 vidua obtus
5	59	36.2	20	2	Q6UQN6	Q6uqn6 vidua hypoc
6	59	36.2	20	2	Q6UQN8	Q6uqn8 vidua macro
7	59	36.2	20	2	Q6UQN9	Q6uqn9 vidua wilso
8	59	36.2	20	2	Q6UQP0	Q6uqp0 vidua camer
9	59	36.2	20	2	Q6UQP2	Q6uqp2 vidua rari
10	59	36.2	20	2	Q6UQP3	Q6uqp3 vidua purpu
11	59	36.2	20	2	Q6UQP4	Q6uqp4 vidua regia
12	59	36.2	20	2	Q6UQP5	Q6uqp5 vidua fisch
13	59	36.2	20	2	AAR12840	Aar12840 vidua fis
14	59	36.2	20	2	AAR12841	Aar12841 vidua reg
15	59	36.2	20	2	AAR12842	Aar12842 vidua pur
16	59	36.2	20	2	AAR12843	Aar12843 vidua rar
17	59	36.2	20	2	AAR12844	Aar12844 vidua rar
18	59	36.2	20	2	AAR12845	Aar12845 vidua cam
19	59	36.2	20	2	AAR12846	Aar12846 vidua wil
20	59	36.2	20	2	AAR12847	Aar12847 vidua mac
21	59	36.2	20	2	AAR12848	Aar12848 vidua mac
22	59	36.2	20	2	AAR12849	Aar12849 vidua hyp
23	59	36.2	20	2	AAR12850	Aar12850 vidua obt
24	59	36.2	20	2	AAR12851	Aar12851 vidua par
25	59	36.2	20	2	AAR12852	Aar12852 vidua ori
26	59	36.2	20	2	AAR12853	Aar12853 anomalosp
27	34	20.9	18	2	Q6XP2	Q6xp2 vitis vinif
28	34	20.9	18	2	AAQ01765	Aa091765 vitis vin
29	33	20.2	19	1	CXAD CONGE	P60274 conus geogr
30	33	20.2	22	2	Q71KS7	Q71ks7 conus stria
31	33	20.2	22	2	AAQ05878	Aa05878 conus str

P12800 canis famil  
Q76br7 homo sapien  
Bac98367 homo sapi  
Q6vix0 bos taurus  
Aar11219 bos tauru  
Aar24093 bos tauru  
O42558 brachydantio  
P36987 plectreurya  
Q788q0 xenopus lae  
Q7ri89 plasmodium  
Q6qvj7 phaseolus v  
Aas18499 phaseolus  
Q7moh0 mus sp. cd3  
P50982 conus ermin

#### ALIGNMENTS

##### RESULT 1

Q6UQN2 PRELIMINARY; PRT; 20 AA.  
ID Q6UQN2  
AC Q6UQN2; 20.2 24 1 PIBG CANFA  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Anomalospiza imberbis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Passeridae;  
OC Anomalospiza.  
OX NCBI\_TaxID=187417;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AY363845; AAR12853.1; -.  
FT NON\_TER 1 1  
FT TER 20 20  
SQ SEQUENCE 20 AA; 2408 MW; 7743B991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNV 11  
| | | | | | | | | |  
DB 10 ALDAAYCFRNV 20

##### RESULT 2

Q6UQN3 PRELIMINARY; PRT; 20 AA.  
ID Q6UQN3  
AC Q6UQN3; 20.2 24 1 PIBG CANFA  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Vidua orientalis aucupum.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Viduinae;  
OC Vidua.  
OX NCBI\_TaxID=247989;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AY363844; AAR12852.1; -.  
FT NON\_TER 1 1  
FT TER 20 20  
SQ SEQUENCE 20 AA; 2408 MW; 7743B991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
 Db 10 ALDAAYCFRNV 20

RESULT 3  
 Q6UQN4 ID Q6UQN4 PRELIMINARY; PRT; 20 AA.  
 AC Q6UQN4;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Transforming growth factor-beta 2 (Fragment)  
 OS Vidua paradisaea (paradise whydah)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
 OC Vidua.  
 OX NCBI\_TaxID=37614;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
 RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
 RL Syst. Biol. 0:0-0(2003).  
 DR EMBL; AY363843; AAR12851.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
 Db 10 ALDAAYCFRNV 20

Query Match 36.2%; Score 59; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
 Db 10 ALDAAYCFRNV 20

RESULT 4  
 Q6UQN5 ID Q6UQN5 PRELIMINARY; PRT; 20 AA.  
 AC Q6UQN5;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Transforming growth factor-beta 2 (Fragment)  
 OS Vidua obtusa (broad-tailed paradise whydah)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
 OC Vidua.  
 OX NCBI\_TaxID=247663;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
 RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
 RL Syst. Biol. 0:0-0(2003).  
 DR EMBL; AY363842; AAR12850.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
 Db 10 ALDAAYCFRNV 20

RESULT 5  
 Q6UQN6 ID Q6UQN6 PRELIMINARY; PRT; 20 AA.  
 AC Q6UQN6;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Transforming growth factor-beta 2 (Fragment)  
 OS Vidua hypocherina.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
 OC Vidua.  
 OX NCBI\_TaxID=187450;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
 RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
 RL Syst. Biol. 0:0-0(2003).  
 DR EMBL; AY363841; AAR12849.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
 Db 10 ALDAAYCFRNV 20

RESULT 6  
 Q6UQN8 ID Q6UQN8 PRELIMINARY; PRT; 20 AA.  
 AC Q6UQN8;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Transforming growth factor-beta 2 (Fragment)  
 OS Vidua macroura.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
 OC Vidua.  
 OX NCBI\_TaxID=187451;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
 RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
 RL Syst. Biol. 0:0-0(2003).  
 DR EMBL; AY363839; AAR12847.1; -.  
 DR EMBL; AY363840; AAR12848.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
 Db 10 ALDAAYCFRNV 20

RESULT 7  
 Q6UQN9 ID Q6UQN9 PRELIMINARY; PRT; 20 AA.  
 AC Q6UQN9;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)



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DE Transforming growth factor-beta 2 (Fragment).
OS Vidua wilsoni (pale-winged indigobird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Viduinae;
OC Vidua.
OX NCBI_TaxID=243222;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AY363836; AAR12846.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNV 11
Db 10 ALDAAAYCFRNV 20

RESULT 8
Q6UQP0 PRELIMINARY; PRT; 20 AA.
AC Q6UQP0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transforming growth factor-beta 2 (Fragment).
OS Vidua camerunensis (Cameroun indigobird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Viduinae;
OC Vidua.
OX NCBI_TaxID=243226;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AY363837; AAR12845.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNV 11
Db 10 ALDAAAYCFRNV 20

RESULT 9
Q6UQP2 PRELIMINARY; PRT; 20 AA.
AC Q6UQP2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transforming growth factor-beta 2 (Fragment).
OS Vidua ruficollis (Jambundu indigobird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Viduinae;
OC Vidua.
OX NCBI_TaxID=243221;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;

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RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AY363835; AAR12843.1; -.
DR EMBL; AY363836; AAR12844.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNV 11
Db 10 ALDAAAYCFRNV 20

RESULT 10
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AC Q6UQP3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transforming growth factor-beta 2 (Fragment).
OS Vidua purpurascens (dusky indigobird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Viduinae;
OC Vidua.
OX NCBI_TaxID=243220;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AY363834; AAR12842.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNV 11
Db 10 ALDAAAYCFRNV 20

RESULT 11
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AC Q6UQP4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transforming growth factor-beta 2 (Fragment).
OS Vidua regia (queen whydah).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Viduinae;
OC Vidua.
OX NCBI_TaxID=243224;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AY363833; AAR12841.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;

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Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
Db 10 ALDAAYCFRNV 20

## RESULT 12

Q6UQPS PRELIMINARY; PRT; 20 AA.  
AC Q6UQPS;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Vidua fischeri (straw-tailed whydah).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
OC Vidua.  
OX NCBI\_TaxID=243223;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AY363832; AAR12840.1; -.  
FT NON TER 1  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
Db 10 ALDAAYCFRNV 20

## RESULT 13

AAR12840 PRELIMINARY; PRT; 20 AA.  
ID AAR12840;  
AC AAR12840;  
DT 02-MAR-2004 (TReMBLrel. 27, Created)  
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Vidua fischeri (straw-tailed whydah).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
OC Vidua.  
OX NCBI\_TaxID=243223;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AY363832; AAR12840.1; -.  
FT NON TER 1  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
Db 10 ALDAAYCFRNV 20

## RESULT 14

AAR12841 PRELIMINARY; PRT; 20 AA.  
ID AAR12841;  
AC AAR12841;  
DT 02-MAR-2004 (TReMBLrel. 27, Created)  
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Vidua regia (queen whydah).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
OC Vidua.  
OX NCBI\_TaxID=243224;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AY363833; AAR12841.1; -.  
FT NON TER 1  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
Db 10 ALDAAYCFRNV 20

## RESULT 15

AAR12842 PRELIMINARY; PRT; 20 AA.  
ID AAR12842;  
AC AAR12842;  
DT 02-MAR-2004 (TReMBLrel. 27, Created)  
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)  
DE Transforming growth factor-beta 2 (Fragment).  
OS Vidua purpurascens (dusky indigobird).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Viduinae;  
OC Vidua.  
OX NCBI\_TaxID=243220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sorenson M.D., Balakrishnan C.N., Payne R.B.;  
RT "Clade-limited colonization in brood parasitic finches (Vidua spp.).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AY363834; AAR12842.1; -.  
FT NON TER 1  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2408 MW; 7743E991CC24BD00 CRC64;

Query Match 36.2%; Score 59; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNV 11  
Db 10 ALDAAYCFRNV 20

Search completed: October 29, 2004, 08:40:39  
Job time : 60 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 08:30:34 ; Search time 152 Seconds  
(without alignments)  
68.442 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 768619

Minimum DB seq length: 0

Maximum DB seq length: 29

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	100.0	29	4	AAG78516 Immunosti
2	150	92.0	27	1	AAP60241 Cartilage
3	121	74.2	21	7	ADC21250 Transform
4	121	74.2	21	7	ADC71237 N-termina
5	102	62.6	29	1	AAP40004 Partial s
6	101	62.0	27	1	AAP60242 Cartilage
7	99	60.7	19	1	AAP95344 N-termina
8	98	60.1	21	7	ADC21251 Transform
9	98	60.1	21	7	ADC71238 N-termina
10	92	56.4	21	7	ADC21252 N-termina
11	92	56.4	21	7	ADC71239 N-termina
12	78	47.9	16	2	AAR08297 TGF-beta
13	78	47.9	16	4	AAG78517 Immunosti
14	78	47.9	28	2	AAW24700 Finger 1
15	75	46.0	17	7	ADC21248 Human TGI
16	75	46.0	17	7	ADC71240 Chromatog
17	75	46.0	21	7	ADC21249 Transform
18	69	42.3	29	1	AAP71611 Fragment
19	68	41.7	21	7	ADC71236 N-termina
20	68	41.7	28	2	AAW24703 Finger 1
21	64	39.3	14	3	AAV92958 Transform
22	63	38.7	28	2	AAW24706 Finger 1
23	61	37.4	28	2	AAW24697 Finger 1
24	61	37.4	28	2	AAW24709 Finger 1
25	58	35.6	12	2	AAW86710 Synthetic

26	57	35.0	16	2	AAK08296 TGF-beta
27	57	35.0	16	4	AAG78522 Immunosti
28	56	34.4	12	2	AAW86721 Synthetic
29	54	33.1	12	2	AAW86711 Synthetic
30	52	31.9	16	2	AAK08295 TGF-beta
31	52	31.9	16	4	AAG78521 Immunosti
32	51	31.3	12	2	AAW86722 Synthetic
33	51	31.3	12	2	AAW86709 Synthetic
34	51	31.3	12	2	AAW86724 Synthetic
35	49	30.1	9	5	AU82694 BP protei
36	49	30.1	9	5	AU82695 BP protei
37	47	28.8	12	2	AAW86712 Synthetic
38	47	28.8	13	3	AAW86712 Human che
39	47	28.8	14	3	AAV92959 Transform
40	46	28.2	12	2	AAW86707 Synthetic
41	46	28.2	12	2	AAW86723 Synthetic
42	46	28.2	13	2	AAV14247 Chemokine
43	46	28.2	13	3	AAW15847 Chemokine
44	46	28.2	13	3	AAW18402 Chemokine
45	46	28.2	14	3	AAV92957 Transform

## ALIGNMENTS

## RESULT 1

AAAG78516

ID AAG78516 standard; peptide; 29 AA.

XX AC AAG78516;

XX XX 22-JAN-2002 (first entry)

XX DE Immunostimulating N-terminal TGF-beta fragment.

XX KW TGF-beta; Transforming growth factor-beta; Immunostimulating; Vaccine;  
 KW Antibody; Cytokine; Immunise.  
 XX OS Homo sapiens.

XX XX WO200172331-A1.

XX XX 04-OCT-2001.

XX PF 30-MAR-2001; 2001WO-DK000218.

XX PR 31-MAR-2000; 2000DK-00000540.

XX PR 13-NOV-2000; 2000US-0246973P.

XX XX (VACC-) VACCINE CHIP TECHNOLOGY AFS.

XX PI Kaastrup P;

XX DR WPI; 2001-639205/73.

XX PT A composition containing a fragment of transforming growth factor-beta  
 with an immunogenic determinant provides increased immunogenicity of the  
 determinant and is useful as a vaccine.  
 XX PS Claim 2; Page 68; 88pp; English.

XX CC The invention relates to an immunogenic composition comprising a fragment  
 of transforming growth factor-beta (TGF-beta) capable of eliciting an  
 immunostimulating effect, and an immunogenic determinant against which  
 the immunogenic response is required. It is believed that when an  
 individual is immunised with a composition comprising the TGF-beta  
 fragment of the invention, antibodies against the fragment are generated.  
 CC Following immunisation, these antibodies may also bind to naturally  
 occurring immunosuppressing cytokines of the immunised individual. This  
 CC may then result in the blocking and/or reduction of the effect of the inhibitory  
 effect of naturally occurring cytokines on the immune system. The TGF-  
 beta fragments of the invention have immunostimulant activity, and as a  
 result may be of use in the manufacture of a medicament for enhancing the

CC immunostimulating effects of an immunisation. The current sequence  
 CC represents the immunostimulating N-terminal TGF-beta fragment  
 XX  
 SQ Sequence 29 AA;

Query Match 100.0%; Score 163; DB 4; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 8e-15; 0; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 0;  
 QY 1 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 29  
 |||||  
 Db 1 ALDAAYCFRNVDNCCCLRPYIDFKRDLG 29  
 |||||

## RESULT 2

AAP60241 standard; peptide; 27 AA.

AC AAP60241;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 24-MAY-1991 (first entry)  
 XX  
 XX Cartilage-inducing factor A.  
 DE  
 XX Cartilage-inducing factor A; implant; chondrogenesis; osteogenesis.  
 KW  
 XX Bos taurus.  
 OS  
 XX EP169016-A.  
 PN  
 XX 22-JAN-1986.  
 PD  
 XX 08-JUL-1985; 85EP-00304848.  
 PF  
 XX 16-JUL-1984; 84US-00630938.  
 PR  
 XX 26-FEB-1985; 85US-00705479.  
 PR  
 XX 19-AUG-1985; 85US-00767144.  
 PR  
 XX 10-DEC-1987; 87US-00130884.  
 PR  
 XX 08-JUN-1988; 88US-00204173.  
 XX  
 XX (CLGE) COLLAGEN CORP.  
 PA  
 XX (CELT-) CELTRIX LABORATORIES INC.  
 PA  
 XX (CELT-) CELTRIX PHARMACEUTICALS INC.

PI Seyedin S, Thomas T;  
 XX  
 XX WPI; 1986-022692/04.  
 DR  
 XX New cartilage-inducing polypeptide(s) - derived from bone, useful in  
 PT implant comps.  
 PT  
 XX Disclosure; Page 16; 27pp; English.

XX Cartilage-inducing factor A is found in mammalian bone, is a co-factor  
 CC for inducing cartilage form., has activity in the TGF-beta assay, and is  
 CC a dimer with mol. wt. ca. 26,000 (SDS-PAGE). It is useful as a component  
 CC for implant comps. for inducing chondrogenesis and osteo- genesis, or  
 CC for promoting connective tissue deposition (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 CC  
 XX Sequence 27 AA;

Query Match 92.0%; Score 150; DB 1; Length 27;  
 Best Local Similarity 96.3%; Pred. No. 4.3e-13; 0; Indels 0; Gaps 0;  
 Matches 26; Conservative 1; Mismatches 0;  
 QY 1 ALDAAYCFRNVDNCCCLRPYIDFKRD 27  
 |||||  
 Db 1 ALDAAYCFRNVDNCCCLRPYIDFKRD 27  
 |||||

## RESULT 3

ADC21250  
 ID ADC21250 standard; peptide; 21 AA.  
 XX  
 AC ADC21250;

XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Transforming growth factor beta2 (TGFbeta2) N-terminal peptide.  
 XX  
 KW Wound healing; burns treatment; TGI; tumour growth inhibitor;  
 KW epithelial cell; human; vulnery; transforming growth factor beta2;  
 KW TGFbeta2.  
 XX  
 OS Homo sapiens.

XX  
 PN US6559123-B1.  
 XX  
 PD 06-MAY-2003.  
 XX  
 XX 22-AUG-1994; 94US-00294061.  
 PF  
 XX 19-APR-1985; 85US-00725003.  
 PR  
 XX 07-APR-1986; 86US-00847931.  
 PR  
 XX 20-OCT-1987; 87US-00111022.  
 PR  
 XX 30-SEP-1991; 91US-00768100.  
 PR  
 XX 04-NOV-1993; 93US-00147904.  
 PR  
 XX 27-JAN-1994; 94US-00188197.  
 XX

PA (OSIP-) OSI PHARM INC.

XX Iwata KK, Stephenson JR, Gold LI;

XX WPI; 2003-729670/69.

PT Treating a wound or burn in a mammal comprises administering a  
 PT homogenous composition comprising a polypeptide prepared by using an  
 PT acidified ethanol extract of human umbilical cord.

XX Disclosure; Fig 15; 86pp; English.

XX The present invention relates to a method for treating a wound or burn in  
 CC a mammal. The method comprises administering a homogenous composition  
 CC comprising a polypeptide known as TGI (tumour growth inhibitor) having a  
 CC molecular weight of 25/26kDa to the mammal, prepared by subjecting an  
 CC acidified ethanol extract of human umbilical cord to hydrophobic  
 CC interaction chromatography and reverse phase high pressure liquid  
 CC chromatography to produce fractions. The homogenous composition is useful  
 CC for treating wounds and burns in a mammal. The composition inhibits the  
 CC growth of mink lung cell line and also inhibits the growth of epithelial  
 CC cells. The present sequence representing the N-terminal peptide of  
 CC transforming growth factor beta2 (TGFbeta2) shows homology to TGI.

XX Sequence 21 AA;

Query Match 74.2%; Score 121; DB 7; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCCLRPY 21  
 |||||  
 Db 1 ALDAAYCFRNVDNCCCLRPY 21  
 |||||

## RESULT 4

ADC71237  
 ID ADC71237 standard; peptide; 21 AA.

XX AC ADC71237;

XX 18-DEC-2003 (first entry)

XX N-terminal transforming growth factor beta 2 peptide.

KW TGF-beta2; transforming growth factor beta 2; tumour growth inhibitor;  
 KW TGI-1; TGI-2; TGI-beta3; wound healing; burn; cytostatic.  
 XX Unidentified.  
 XX US5586394-B1.  
 PN XX  
 XX 01-JUL-2003.  
 PD XX  
 PF 27-JAN-1994; 94US-00188197.  
 XX XX  
 PR 19-APR-1985; 85US-00725003.  
 PR 07-APR-1986; 86US-00847931.  
 PR 20-OCT-1986; 86US-00922121.  
 PR 20-OCT-1987; 87US-00111022.  
 PR 30-SEP-1991; 91US-00768100.  
 PR 04-NOV-1993; 93US-00147904.  
 XX XX  
 PA (OSIP-) OSI PHARM INC.  
 XX XX  
 PI Iwata KK, Stephenson JR, Goid LI;  
 XX XX  
 DR WPI; 2003-719694/68.  
 XX XX

PT New homogeneous polypeptide composition, useful for inhibiting growth of  
 PT a mink lung cell line, for treating burn or for promoting wound healing.  
 XX  
 PS Disclosure; Fig 15; 72pp; English.  
 XX XX  
 CC This invention relates to a novel chromatographically recovered  
 CC polypeptide identified as tissue derived tumour growth inhibitor (TGI),  
 CC also known as TGI-1, TGI-2 and TGI-beta3. Specifically, the inhibitory  
 CC activity can be used against human tumour cells and an established mink  
 CC lung cell line (CCL64), while stimulating the growth of normal human  
 CC foreskin fibroblasts. As such, the present invention describes  
 CC pharmaceutical compositions consisting of the cytostatic TGI peptide,  
 CC which can be used to inhibit the growth of epithelial cells, promote  
 CC wound healing or for treatment of burns. This peptide sequence is the N-  
 CC terminal peptide region of the TGF-beta2 (transforming growth factor beta  
 CC 2), which is homologous to the TGI peptide of the invention.  
 XX XX  
 SQ Sequence 21 AA;

Query Match 74.2%; Score 121; DB 7; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAFCFRNVQDNCCLRPY 21  
 Db 1 ALDAAFCFRNVQDNCCLRPY 21  
 RESULT 5  
 AAP40004  
 ID AAP40004 standard; protein; 29 AA.  
 AC AAP40004;  
 XX XX  
 XX 25-MAR-2003 (revised)  
 DT 30-NOV-1991 (first entry)  
 DE Partial sequence of beta-type transforming growth factor.  
 XX Beta-type transforming growth factor; platelet; placenta.  
 KW Homo sapiens.  
 XX EP128849-A.  
 XX 19-DEC-1984.  
 PD 04-JUN-1984; 84EP-00450016.  
 PF XX  
 XX

PR 03-JUN-1983; 83US-00500832.  
 PR 03-JUN-1983; 83US-00500927.  
 XX (USDC ) US SEC OF COMMERCE.  
 PA Frolik CA, Assolan RK, Sporn MB, Roberts AB;  
 XX WPI; 1984-314215/51.  
 DR XX  
 XX Purified beta-type trans-forming growth factors - prepd. from human blood  
 PT platelets and human placenta.  
 PT Disclosure; Page 26; 32pp; English.  
 XX XX

CC The peptide is a partial sequence of beta-type transforming growth factor  
 CC (bTGF) isolated from human placenta. C-S-carboxymethylcysteine and  
 CC X-undetermined. bTGF is different from platelet-derived growth factor and  
 CC has a mol. wt. of 25,000. Unlike most growth factors, it does not exert  
 CC its growth promoting property by direct stimulation of total DNA  
 CC synthesis. bTGF from human placenta does not compete with epidermal  
 CC growth factor for membrane receptor sites, but is does require bGF  
 CC induction of anchorage-independent growth of indicator cells. bTGF may  
 CC play a unique role in physiological and pathological processes where  
 CC platelet-derived factors modulate cell proliferation, since it has strong  
 CC growth promoting activity but is not a strong mitogen. (Updated on 25-MAR  
 CC -2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX XX  
 SQ Sequence 29 AA;

Query Match 62.6%; Score 102; DB 1; Length 29;  
 Best Local Similarity 58.6%; Pred. No. 1.4e-06;  
 Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLG 29  
 Db 1 ALDTCFSSSTKNCVCCVQLYIDFKXDLG 29  
 RESULT 6  
 AAP60242  
 ID AAP60242 standard; protein; 27 AA.  
 XX XX  
 AC AAP60242;  
 XX XX  
 DT 25-MAR-2003 (revised)  
 DT 24-MAY-1991 (first entry)  
 XX XX  
 DE Cartilage-inducing factor B.  
 XX Cartilage-inducing factor B; implant; chondrogenesis; osteogenesis.  
 KW Bos taurus.  
 XX EP169016-A.  
 XX 22-JAN-1986.  
 PD 08-JUL-1985; 85EP-00304848.  
 PF 16-JUL-1984; 84US-00630938.  
 PR 26-FEB-1985; 85US-00705479.  
 PR 19-AUG-1985; 85US-00767144.  
 PR 10-DEC-1987; 87US-00130884.  
 PR 08-JUN-1988; 88US-00204173.  
 XX (CLGE ) COLLAGEN CORP.  
 PA (CELT-) CELTRIX LABORATORIES INC.  
 PA (CELT-) CELTRIX PHARMACEUTICALS INC.  
 XX Seyedin S, Thomas T;  
 PI WPI; 1986-022692/04.  
 DR XX  
 XX

PT	New cartilage-inducing polypeptide(s) - derived from bone, useful in
PT	implant compns.
XX	
XX	Disclosure; Page 14; 27pp; English.
XX	
CC	Cartilage-inducing factor B is found in mammalian bone, is a co-factor
CC	for inducing cartilage formn., has activity in the TGF-beta assay, and is
CC	a dimer with mol. wt. ca. 26,000 (SDS-PAGE). It is useful as a component
CC	for implant compns. for inducing chondrogenesis and osteo- genesis, or
CC	for promoting connective tissue deposition (Updated on 25-MAR-2003 to
CC	correct PA field.)
XX	
XX	Sequence 27 AA:
SO	

```

Query Match      62.0%; Score 101; DB 1; Length 27;
Best Local Similarity 59.3%; Pred. No. 1.8e-06;
Matches 16; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNVDNCCLRPLYYIDFKRD 27
      ||||| : ||||| : ||||| :
Db 1 ALDNYACFSSTKKCCVCCVYYIDFKRD 27

```

RESULT 7	
AA95344	
ID	ADP95344 standard; peptide; 19 AA.
XX	
XX	
AC	AA95344;
XX	
XX	
DT	26-JUL-1989 (first entry)
XX	
DE	
DE	N-terminal of the Milk Growth Factor (MGF).
XX	
KW	Milk Growth Factor; Epidermal Growth Factor.

Query Match 60.7%; Score 99; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.4e-06;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ALDAAYCFRNVQDNCCLRP	19
Db	1	ALDAAYCFRNVQDNCCXXP	19

RESULT 8  
ADC21251  
ID ADC21251 standard; peptide; 21 AA.  
XX  
XX ADC21251;  
XX AC  
XX AC  
DT 18-DEC-2003 (first entry)

Query Match 60.1%; Score 98; DB 7; Length 21;  
Best Local Similarity 71.4%; Pred. NO. 3.6e-06;  
Matches 15; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT 9  
ADC71238  
ID ADC71238 standard; peptide; 21 AA.

```

XX AC ADC71238;
XX DT 18-DEC-2003 (first entry)
XX DE N-terminal transforming growth factor beta 3 peptide.
XX KW TGF-beta3; transforming growth factor beta 3; tumour growth inhibitor;
XX KW TGI; TGI-1; TGI-2; TGI-beta3; wound healing; burn; cytostatic.
XX OS Unidentified.
XX FN US6586394-B1.
XX PD 01-JUL-2003.
XX PF 27-JAN-1994; 94US-00188197.
XX PR 19-APR-1985; 85US-00725003.
XX PR 07-APR-1986; 86US-00847931.
XX PR 20-OCT-1986; 86US-00922121.
XX PR 20-OCT-1987; 87US-00111022.
XX PR 30-SEP-1991; 91US-00768100.
XX PR 04-NOV-1993; 93US-00147904.
XX PA (OSIP-) OSI PHARM INC.
XX PI Iwata KK, Stephenson JR, Gold LI;
XX WI; 2003-719694/68.
XX PT New homogeneous polypeptide composition, useful for inhibiting growth of
XX PT a mink lung cell line, for treating burn or for promoting wound healing.
XX PS Disclosure; Fig 15; 72pp; English.
XX CC This invention relates to a novel chromatographically recovered
XX CC polypeptide identified as tissue derived tumour growth inhibitor (TGI),
XX CC also known as TGI-1, TGI-2 and TGI-beta3. Specifically, the inhibitory
XX CC activity can be used against human tumour cells and an established mink
XX CC lung cell line (CCU64), while stimulating the growth of normal human
XX CC foreshin fibroblasts. As such, the present invention describes
XX CC pharmaceutical compositions consisting of the cytostatic TGI peptide,
XX CC which can be used to inhibit the growth of epithelial cells, promote
XX CC wound healing or for treatment of burns. This peptide sequence is the N-
XX CC terminal peptide region of the TGF-beta3 (transforming growth factor beta
XX CC 3), which is homologous to the TGI peptide of the invention.
XX SQ Sequence 21 AA;
Query Match 60.1%; Score 98; DB 7; Length 21;
Best Local Similarity 71.4%; Pred. No. 3.6e-06;
Matches 15; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALDAAVCFRNVDNCCLRPLY 21
DB 1 ALDNTYCFRNLENCVVRPLY 21
RESULT 10
ADC21252
ID ADC21252 standard; peptide; 21 AA.
XX AC ADC21252;
XX DT 18-DEC-2003 (first entry)
XX DE N-terminal peptide of tumour growth inhibitor (TGI).
XX KW Wound healing; burns treatment; TGI; tumour growth inhibitor;
XX KW epithelial cell; human; vulnerary.
XX OS Homo sapiens.

```

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XX PH Key Location/Qualifiers
XX FT Misc-difference 18 /label= Unknown
XX FN US6559123-B1.
XX PD 06-MAY-2003.
XX PF 22-AUG-1994; 94US-00294061.
XX PR 19-APR-1985; 85US-00725003.
XX PR 07-APR-1986; 86US-00847931.
XX PR 20-OCT-1987; 87US-00111022.
XX PR 30-SEP-1991; 91US-00768100.
XX PR 04-NOV-1993; 93US-00147904.
XX PR 27-JAN-1994; 94US-00188197.
XX PA (OSIP-) OSI PHARM INC.
XX PI Iwata KK, Stephenson JR, Gold LI;
XX WI; 2003-729670/69.
XX PT Treating a wound or burn in a mammal comprises administering a
XX PT homogeneous composition comprising a polypeptide prepared by using an
XX PT acidified ethanol extract of human umbilical cord.
XX PS Disclosure; Fig 15; 86pp; English.
XX CC The present invention relates to a method for treating a wound or burn in
XX CC a mammal. The method comprises administering a homogeneous composition
XX CC comprising a polypeptide known as TGI (tumour growth inhibitor) having a
XX CC molecular weight of 25/26kDa to the mammal, prepared by subjecting an
XX CC acidified ethanol extract of human umbilical cord to hydrophobic
XX CC interaction chromatography and reverse phase high pressure liquid
XX CC chromatography to produce fractions. The homogeneous composition is useful
XX CC for treating wounds and burns in a mammal. The composition inhibits the
XX CC growth of mink lung cell line and also inhibits the growth of epithelial
XX CC cells. The present sequence represents the N-terminal peptide of human
XX CC TGI.
XX SQ Sequence 21 AA;
Query Match 56.4%; Score 92; DB 7; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e-05;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 ALDAAVCFRNVDNCCLRPLY 21
DB 1 ALDNTYCFRNLENCVVRPLY 21
RESULT 11
ADC71239
ID ADC71239 standard; peptide; 21 AA.
XX AC ADC71239;
XX DT 18-DEC-2003 (first entry)
XX DE N-terminal tissue derived tumour growth inhibitor (TGI) peptide.
XX KW tumour growth inhibitor; TGI; TGI-1; TGI-2; TGI-beta3; wound healing;
XX KW burn; cytostatic.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX FT Misc-difference 18 /label= Xaa
XX FT /note= "Xaa= unknown"
XX FT

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PN US6586394-B1.  
 XX  
 PD 01-JUL-2003.  
 XX  
 PF 27-JAN-1994; 94US-00188197.  
 XX  
 PR 19-APR-1985; 85US-00725003.  
 PR 07-APR-1986; 86US-00847931.  
 PR 20-OCT-1986; 86US-00922121.  
 PR 20-OCT-1987; 87US-00111022.  
 PR 30-SEP-1991; 91US-00768100.  
 PR 04-NOV-1993; 93US-00147904.  
 XX  
 PA (OSIP-) OSI PHARM INC.  
 XX  
 PI Iwata KK, Stephenson JR, Gold LI;  
 XX  
 DR WPI; 2003-719694/68.  
 XX  
 PT New homogeneous polypeptide composition, useful for inhibiting growth of  
 PT a mink lung cell line, for treating burn or for promoting wound healing.  
 XX  
 PS Disclosure; Fig 15; 72pp; English.  
 XX  
 CC This invention relates to a novel chromatographically recovered  
 CC polypeptide identified as tissue derived tumour growth inhibitor (TGI),  
 CC also known as TGI-1, TGI-2 and TGI-beta3. Specifically, the inhibitory  
 CC activity can be used against human tumour cells and an established mink  
 CC lung cell line (CC64), while stimulating the growth of normal human  
 CC foreskin fibroblasts. As such, the present invention describes  
 CC pharmaceutical compositions consisting of the cytostatic TGI peptide,  
 CC which can be used to inhibit the growth of epithelial cells, promote  
 CC wound healing or for treatment of burns. This peptide sequence is the N-  
 CC terminal peptide region of the tissue derived tumour growth inhibitor  
 CC (TGI) of the invention.  
 XX  
 SQ Sequence 21 AA;  
 Query Match 56.4%; Score 92; DB 7; Length 21;  
 Best Local Similarity 66.7%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ALDAAYCFRNQDNCCLRPY 21  
 DB 1 ALDTNYCFRNLEENCCVXPY 21  
 RESULT 12  
 AAR08297  
 ID AAR08297 standard; protein; 16 AA.  
 XX  
 AC AAR08297;  
 XX  
 DT 09-JAN-2003 (revised)  
 DT 04-MAR-1991 (first entry)  
 XX  
 DE TGF-beta based peptide (III) as immunosuppressive.  
 XX  
 KW TGF-beta; organ resection; septic shock; autoimmune disease;  
 KW rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC9014359-A.  
 XX  
 PD 29-NOV-1990.  
 XX  
 PF 25-MAY-1989; 89US-00356964.  
 XX  
 PR 25-MAY-1989; 89US-00356964.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX

PI Burnier JA;  
 XX  
 DR WPI; 1990-375948/50.  
 XX  
 PT New polypeptide(s) and compans. based on TGF-beta - used for treatment of  
 PT organ resection, septic shock, auto-immune disease, rheumatoid arthritis  
 PT etc.  
 XX  
 PS Claim 12; Page 31; 47pp; English.  
 XX  
 CC The sequence is based on conserved sequences in the family of TGF-beta  
 CC molecules. The polypeptide may be prepared by solid phase synthesis.  
 CC fragment condensation or recombinant DNA technique and has TGF-beta-like  
 CC activity. It can be used for treating immune or inflammatory disorders,  
 CC e.g. allograft rejection, septic shock, adult respiratory disease  
 CC syndrome, autoimmune disease rheumatoid arthritis, systemic lupus  
 CC erythematosus or inflammatory bowel disease. They can also be used in  
 CC wound healing and as immunogens to elicit antibodies. See also AAR08295-  
 CC 97. (Updated on 09-JAN-2003 to add missing OS field.)  
 XX  
 SQ Sequence 16 AA;  
 Query Match 47.9%; Score 78; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0014;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 CLRPLXIDFKRDIG 29  
 DB 1 CLRPLXIDFKRDIG 14  
 RESULT 13  
 AAG78517  
 ID AAG78517 standard; peptide; 16 AA.  
 XX  
 AC AAG78517;  
 XX  
 DT 22-JAN-2002 (first entry)  
 DE Immunostimulating TGF-beta fragment 1.  
 XX  
 KW TGF-beta; Transforming growth factor-beta; Immunostimulating; Vaccine;  
 KW Antibody; Cytokine; Immunise.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200172331-A1.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-DK000218.  
 XX  
 PR 31-MAR-2000; 2000DK-00000540.  
 PR 13-NOV-2000; 2000US-0246973P.  
 XX  
 PA (VACC-) VACCINE CHIP TECHNOLOGY APS.  
 XX  
 PI Kaastrup P;  
 XX  
 DR WPI; 2001-639205/73.  
 XX  
 PT A composition containing a fragment of transforming growth factor-beta  
 PT with an immunogenic determinant provides increased immunogenicity of the  
 PT determinant and is useful as a vaccine.  
 XX  
 PS Disclosure; Page 83; 88pp; English.  
 XX  
 CC The invention relates to an immunogenic composition comprising a fragment  
 CC of transforming growth factor-beta (TGF-beta) capable of eliciting an  
 CC immunostimulating effect, and an immunogenic determinant against which  
 CC the immunogenic response is required. It is believed that when an  
 CC individual is immunised with a composition comprising the TGF-beta  
 CC fragment of the invention, antibodies against the fragment are generated.

App



CC Following immunisation, these antibodies may also bind to naturally  
CC occurring immunosuppressing cytokines of the immunised individual. This  
CC may then result in the blocking and/or reduction of the of the inhibitory  
CC effect of naturally occurring cytokines on the immune system. The TGF-  
CC beta fragments of the invention have immunostimulant activity, and as a  
CC result may be of use in the manufacture of a medicament for enhancing the  
CC immunostimulating effects of an immunisation. The current sequence  
CC represents the immunostimulating TGF-beta fragment 1  
XX  
XX Sequence 16 AA;  
SQ

Query Match 47.9%; Score 78; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CLRPLYIDFKRDLG 29  
DB 1 CLRPLYIDFKRDLG 14

RESULT 14  
AAW24700  
ID AAW24700 standard; peptide; 28 AA.  
XX  
XX AAW24700;  
AC  
XX  
DT 02-OCT-1997 (first entry)  
XX  
DE Finger 1 domain of TGF-beta2.  
XX  
KW Finger 1; domain; transforming growth factor-beta1; TGF-beta1; agonist;  
KW biopolymer; F1; finger 2; F2; heel; ligand binding surface; mimic;  
KW TGF-beta superfamily; receptor; analogue; morphon; cell surface receptor;  
KW morphogenic cascade.  
XX  
XX Homo sapiens.  
XX WO9640771-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009293.  
XX  
PR 07-JUN-1995; 95US-00478097.  
XX  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
XX  
PI Keck PC, Smart JE;  
XX  
XX WPI; 1997-087054/08.  
DR  
XX  
XX Transforming growth factor (TGF)-beta single chain analogues - bind to  
XX natural TGF-beta receptors, esp. to activate a morphogenic cascade.  
PT  
XX Claim 6; Page 71-72; 134pp; English.

CC This sequence represents the finger 1 domain of transforming growth  
CC factor (TGF)-beta2 which corresponds to residues 2-29. This peptide was  
CC used as part of a single chain synthetic amino acid biopolymer construct  
CC which contains a finger 1 (F1), a finger 2 (F2) and a heel (H) region  
CC together which are complementary to the ligand binding surface of a TGF-  
CC beta superfamily receptor, and an amino acid structure which mimics the  
CC structure of a member of the TGF-beta superfamily, such that the  
CC construct preferentially binds the receptor. The new single stranded TGF-  
CC beta superfamily analogues are designated morphons; they bind  
CC preferentially, either in vivo or in vitro, to a natural cell surface  
CC receptor for the TGF-beta superfamily member they are derived from. Upon  
CC binding to the receptor, the analogues can act as agonists or mimics of  
CC the parent TGF-beta superfamily member activity, pref. by activating a  
CC morphogenic cascade. The new TGF-beta family analogues are thought to  
CC have a lower molecular weight than the natural dimers and will therefore  
CC have a faster rate of diffusion. The morphons may be engineered to  
CC enhance their binding activity

XX  
SQ Sequence 28 AA;  
XX  
Query Match 47.9%; Score 78; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CLRPLYIDFKRDLG 29  
DB 1 CLRPLYIDFKRDLG 14

RESULT 15  
ADC21248  
ID ADC21248 standard; peptide; 17 AA.  
XX  
XX ADC21248;  
AC  
XX  
DT 18-DEC-2003 (first entry)  
XX  
XX Human TGI peptide useful for treating burns/wounds.  
XX  
KW Wound healing; burns treatment; TGI; tumour growth inhibitor;  
KW epithelial cell; human; vulnerary.  
XX  
XX Homo sapiens.  
XX US6559123-B1.  
XX  
PD 06-MAY-2003.  
XX  
PF 22-AUG-1994; 94US-00294061.  
XX  
PR 19-APR-1985; 85US-00725003.  
PR 07-APR-1986; 86US-00847931.  
PR 20-OCT-1987; 87US-00111022.  
PR 30-SEP-1991; 91US-00768100.  
PR 04-NOV-1993; 93US-00147904.  
PR 27-JAN-1994; 94US-00188197.  
XX  
XX (OSIP-) OSI PHARM INC.  
XX  
XX Iwata KK, Stephenson JR, Gold LI;  
XX  
XX WPI; 2003-729670/69.  
XX  
XX Treating a wound or burn in a mammal comprises administering a  
XX PT homogenous composition comprising a polypeptide prepared by using an  
XX PT acidified ethanol extract of human umbilical cord.  
XX  
XX Disclosure; Col 2; 86pp; English.

CC The present invention relates to a method for treating a wound or burn in  
CC a mammal. The method comprises administering a homogenous composition  
CC comprising a polypeptide known as TGI (tumour growth inhibitor) having a  
CC molecular weight of 25/26kDa to the mammal, prepared by subjecting an  
CC acidified ethanol extract of human umbilical cord to hydrophobic  
CC interaction chromatography and reverse phase high pressure liquid  
CC chromatography to produce fractions. The homogenous composition is useful  
CC for treating wounds and burns in a mammal. The composition inhibits the  
CC growth of milk lung cell line and also inhibits the growth of epithelial  
CC cells. The present sequence represents a human TGI peptide useful for  
CC treating burns/wounds.

XX  
SQ Sequence 17 AA;  
XX  
Query Match 46.0%; Score 75; DB 7; Length 17;  
Best Local Similarity 64.7%; Pred. No. 0.0038;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCL 17  
DB 1 ALDTNCFRNLENCV 17

Search completed: October 29, 2004, 08:39:35  
Job time : 154 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2004, 08:31:29 ; Search time 37 seconds  
(without alignments)

75.413 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 5939

Minimum DB seq length: 0

Maximum DB seq length: 29

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR79.\*

2: PIR1.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	26.4	19	2	A21182
2	41	25.2	20	2	JT0410
3	40	24.5	19	2	C21182
4	35.5	21.8	27	2	A58997
5	34	20.9	16	2	PH1778
6	33.5	20.6	24	2	A37973
7	33	20.2	24	2	A5298
8	30	18.4	24	2	E33613
9	29	17.8	17	2	I53392
10	29	17.8	18	1	A58589
11	28.5	17.5	28	2	S41774
12	28	17.2	26	2	B37119
13	28	17.2	26	2	I57726
14	28	17.2	27	1	A58175
15	28	17.2	29	2	A43620
16	28	17.2	29	2	B43620
17	27.5	16.9	27	2	S19619
18	27	16.6	15	2	D48394
19	27	16.6	17	2	A38824
20	27	16.6	17	2	JU0125
21	27	16.6	18	2	JU0125
22	27	16.6	19	2	JU0124
23	27	16.6	24	2	A05134
24	26.5	16.3	29	2	A58537
25	26	16.0	17	2	I49425
26	26	16.0	18	2	JU0124
27	26	16.0	27	2	A1412
28	25.5	15.6	25	2	JU0701
29	25.5	15.6	26	1	NTSR3L

30	25	15.3	10	2	PC2171
31	25	15.3	10	2	I52645
32	25	15.3	11	2	S78765
33	25	15.3	15	2	PH1613
34	25	15.3	17	2	A35550
35	25	15.3	18	2	PQ0022
36	25	15.3	21	2	H64640
37	25	15.3	24	2	A60606
38	25	15.3	29	2	S01614
39	25	15.3	29	2	H89949
40	24.5	15.0	25	2	C35507
41	24.5	15.0	25	2	JU0700
42	24	14.7	11	2	S04875
43	24	14.7	13	2	PH1593
44	24	14.7	16	2	A59046
45	24	14.7	16	2	A59045

ALIGNMENTS

RESULT 1

A21182  
4K prothoracicotropic hormone I - silkworm (fragment)  
C;Species: Bombyx mori (silkworm)

C;Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 09-Jul-2004  
C;Accession: A21182

R;Nagasawa, H.; Kataoka, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.; Mizoguchi, S.

Science 226, 1344-1345, 1984

A;Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone:

A;Reference number: A21182

A;Accession: A21182

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <NAG>

A;Cross-references: UNIPROT:P26733

C;Superfamily: insulin

Query Match 26.4%; Score 43; DB 2; Length 19;

Best Local Similarity 53.8%; Pred. No. 11;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 11 VQDNCCLRPYID 23

Db 2 VDECCCFRPTLD 14

RESULT 2

JT0410

bombyxin-IV chain A - silkworm

C;Species: Bombyx mori (silkworm)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 20-Mar-1998

C;Accession: JT0410

R;Maruyama, K.; Hietter, H.; Nagasawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.

Agric. Biol. Chem. 52, 3035-3041, 1988

A;Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of b

A;Reference number: JT0410

A;Accession: JT0410

A;Molecule type: protein

A;Residues: 1-20 <MAR>

C;Superfamily: insulin

F;6-11/Disulfide bonds: #status predicted

F;7/Disulfide bonds: interchain (to chain B-10) #status predicted

F;20/Disulfide bonds: interchain (to chain B-22) #status predicted

Query Match 25.2%; Score 41; DB 2; Length 20;

Best Local Similarity 46.2%; Pred. No. 22;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 11 VQDNCCLRPYID 23

Db 2 VDECCCFRPTLD 14

## RESULT 3

C21182  
4K prothoracicotropic hormone III - silkworm (fragment)  
C:Species: Bombyx mori (silkworm)  
C:Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 12-Apr-1995  
C:Accession: C21182  
R:Nagasawa, H.; Kataoka, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.; Mizoguchi, S.  
A:Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone.  
A:Reference number: A21182  
A:Accession: C21182  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <NAG>  
C:Superfamily: insulin

Query Match 24.5%; Score 40; DB 2; Length 19;  
Best Local Similarity 53.8%; Pred. No. 29;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 11 VQDNCCLRPLYID 23  
| | | | |  
DB 2 VVDECCLOPCTXD 14  
| | | | |

## RESULT 4

A58997  
kappa-conotoxin PVIIA - cone shell (Conus purpurascens)  
N:Alternate names: fin-popping peptide  
C:Species: Conus purpurascens (purple cone)  
C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: A58997  
R:Terlau, H.; Shon, K.J.; Grille, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M.  
A:Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail.  
A:Reference number: A58997  
A:Accession: A58997  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-27 <TER>  
A:Cross-references: UNIPROT:P56633  
C:Comment: This conotoxin blocks conductance of the Shaker potassium channel.  
C:Keywords: hydroxyproline; neurotoxin; venom  
F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 21.8%; Score 35.5; DB 2; Length 27;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 7 CPERNVQDNCLR 18  
| | | | |  
DB 8 CFQHL-DDCCSR 18  
| | | | |

## RESULT 5

PH1778  
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1778  
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057  
A:Accession: PH1778  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-16 <POR>

Query Match 20.9%; Score 34; DB 2; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 15 CCLRPLYIDPK 25  
| | | | |  
DB 3 CWRPTFNDYK 13  
| | | | |

## RESULT 6

A37973  
lutropin-choriogonadotropin receptor - rat (fragment)  
N:Alternate names: luteinizing hormone-choriogonadotropin receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jun-1991 #sequence\_revision 21-Jun-1991 #text\_change 23-Feb-1996  
C:Accession: A37973  
R:Tesai-Morris, C.H.; Buczko, E.; Wang, W.; Dufau, M.L.  
J. Biol. Chem. 265, 19385-19388, 1990  
A:Title: Intronic nature of the rat luteinizing hormone receptor gene defines a soluble  
A:Reference number: A37973; MUID:91060531; PMID:2174034  
A:Accession: A37973  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-24 <TSA>

Query Match 20.8%; Score 33.5; DB 2; Length 24;  
Best Local Similarity 40.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

QY 1 ALDAAYCFRNVQDNCCLRPL 20  
| | | | |  
DB 7 ALPAAHCLRLGLPNK---RPV 23  
| | | | |

## RESULT 7

A05298  
fibrinogen gamma chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C:Accession: A05298  
R:Birken, S.; Wilner, G.D.; Canfield, R.E.  
Thromb. Res. 7, 599-610, 1975  
A:Title: Studies of the structure of canine fibrinogen.  
A:Reference number: A94308; MUID:76081726; PMID:1198547  
A:Accession: A05298  
A:Molecule type: protein  
A:Residues: 1-24 <BIR>  
A:Cross-references: UNIPROT:P12800  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
C:Keywords: blood coagulation; liver; plasma

Query Match 20.2%; Score 33; DB 2; Length 24;  
Best Local Similarity 66.7%; Pred. No. 3.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 QDNCCCL 17  
| | | | |  
DB 5 RDNCCI 10  
| | | | |

## RESULT 8

E53613  
plectoxin XIII - spider (Plectreureys tristis)  
C:Species: Plectreureys tristis  
C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: E53613  
R:Quistad, G.B.; Skinner, W.S.  
J. Biol. Chem. 269, 11098-11101, 1994  
A:Title: Isolation and sequencing of insecticidal peptides from the primitive hunting sp

A:Reference number: A53613; MUID:94209277; PMID:8157635  
A:Accession: E53613  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-24 <QUI>  
A:Cross-references: UNIPROT:P36987

C;Superfamily: curtatoxin

Query Match 16.4%; Score 30; DB 2; Length 24;  
Best Local Similarity 54.5%; Pred. No. 9.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 1;

QY 6 YCFRNVDNCC 16  
|||  
DB 10 YCNGNVE--CC 18

## RESULT 9

I53392  
CD33 antigen homolog - mouse (fragment)  
C;Species: Mus sp. (mouse)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I53392

R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.

Eur. J. Immunol. 24, 1657-1664, 1994

A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is r

A;Reference number: I53392; MUID:94298870; PMID:8026526

A;Accession: I53392

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-17 <RES>

A;Cross-references: UNIPROT:Q7M0H0; GB:S71347; NID:G550035

C;Genetics:

A;Gene: Ig VHx24b

Query Match 17.8%; Score 29; DB 2; Length 17;  
Best Local Similarity 57.1%; Pred. No. 9.8e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0;

QY 16 CLRPLYI 22  
|||  
DB 2 CARPYIV 8

## RESULT 10

A58589  
alpha-conotoxin EI - cone shell (Conus ermineus)

C;Species: Conus ermineus (ermine cone)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: A58589

R;Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;

Biochemistry 34, 14519-14526, 1995

A;Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nove

A;Reference number: A58589; MUID:96062516; PMID:7578057

A;Accession: A58589

A;Molecule type: protein

A;Residues: 1-18 <WAK>

A;Cross-references: UNIPROT:P50982

A;Note: sequence confirmed by chemical synthesis

C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt

C;Superfamily: This alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos

F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;4-10,5-18/Disulfide bonds: #status experimental

F;18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 17.8%; Score 29; DB 1; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 QDNCCLRP 19  
|||  
DB 1 RDPCCYHP 8

## RESULT 11

S41774

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Trypanosoma congolense mit

C;Species: mitochondrion Trypanosoma congolense

C;Date: 25-Dec-1994 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C;Accession: S41774

R;Read, L.K.; Fish, W.R.; Murbiani, A.M.; Stuart, K.

Nucleic Acids Res. 21, 4073-4078, 1993

A;Title: Maxicircle DNA and edited mRNA sequences of closely related trypanosome species;

A;Reference number: S41774; MUID:93382785; PMID:8396763

A;Accession: S41774

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-28 <REA>

A;Cross-references: UNIPROT:Q7M2D7

C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; piastquinol

C;Keywords: electron transfer; mitochondrion; oxidative phosphorylation; oxidoreductase

Query Match 17.5%; Score 28.5; DB 2; Length 28;  
Best Local Similarity 60.0%; Pred. No. 1.8e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 8 FRNVQDNCC 17  
|||  
DB 13 FRNL---CCL 19

## RESULT 12

B37119

acetyl-CoA carboxylase (EC 6.4.1.2) (clone lambdaDHN59) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 19-Mar-1999

C;Accession: B37119

R;Kong, I.S.; Lopez-Casillas, F.; Kim, K.H.

J. Biol. Chem. 265, 13695-13701, 1990

A;Title: Acetyl-CoA carboxylase mRNA species with or without inhibitory coding sequence

A;Reference number: A37119; MUID:90337981; PMID:1974251

A;Accession: B37119

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-26 <KON>

A;Cross-references: GB:M55315

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin

C;Keywords: ligase

Query Match 17.2%; Score 28; DB 2; Length 26;  
Best Local Similarity 44.4%; Pred. No. 2e+03;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 RNVDNCC 17  
|||  
DB 2 ROLKDNCTV 10

## RESULT 13

I57726

major outer membrane protein A(3b) - Escherichia coli

C;Species: Escherichia coli

C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004

C;Accession: I57726

R;Gordon, G.; Gayda, R.C.; Markovitz, A.

Mol. Gen. Genet. 193, 414-421, 1984

A;Title: Sequence of the regulatory region of omp T, the gene specifying major outer mem

A;Reference number: I57726; MUID:84167352; PMID:6323918

A;Accession: I57726

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-26 <RES>

A;Cross-references: UNIPROT:Q47416; EMBL:X00348; NID:G42163; PIDN:CAA25097.1; PID:94216

Query Match 17.2%; Score 28; DB 2; Length 26;  
Best Local Similarity 31.6%; Pred. No. 2e+03;  
Matches 6; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

QY 6 YCFRNVDNCCLRPLYIDF 24  
|||  
DB 9 FCTKNI-----VLRITFFDF 23

```

RESULT 14
A58175
delta-conotoxin TxVIIA - cone shell (Conus textile)
N/Alternate names: conotoxin TxVIIA
C/Species: Conus textile (cloth-of-gold cone)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A58175; S19620
R/Nakamura, T.; Yu, Z.; Fainzilber, M.; Burlingame, A.L.
Protein Sci. 5, 524-530, 1996
A/Title: Mass spectrometric-based revision of the structure of a cysteine-rich peptide
A/Reference number: A58175; MUID:97022130; PMID:8868490
A/Contents: correction
A/Accession: A58175
A/Molecule type: protein
A/Residues: 1-27 <NAK>
A/Cross-references: UNIPROT:P24160
R/Fainzilber, M.; Gordon, D.; Hasson, A.; Spira, M.E.; Zlotkin, E.
Eur. J. Biochem. 202, 589-595, 1991
A/Title: Mollusc-specific toxins from the venom of Conus textile neovivarius.
A/Reference number: S19553; MUID:92104183; PMID:1761058
A/Accession: S19620
A/Molecule type: protein
A/Residues: 'W', 2-25 <PAI>
C/Superfamily: omega-conotoxin
C/Keywords: amidated carboxyl end; carboxylglutamic acid; neurotoxin; sodium channel inh
F;1-15,8-19,14-24/Disulfide bonds: #status predicted
F;9,13/Modified site: gamma-carboxylglutamic acid (Glu) #status experimental
F;27/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 17.2%; Score 28; DB 1; Length 27;
Best Local Similarity 38.5%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 4 AAYCFRNVDNCC 16
: |||
Db 5 STYC--EVDSECC 15

RESULT 15
A43620
omega-conotoxin GVIIA - cone shell (Conus geographus)
N/Alternate names: shaker peptide GVIIA
C/Species: Conus geographus (geography cone)
C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C/Accession: A43620
R/Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Sant
Science 230, 1338-1343, 1985
A/Title: Peptide neurotoxins from fish-hunting cone snails.
A/Reference number: A43620; MUID:86070213; PMID:4071055
A/Accession: A43620
A/Molecule type: protein
A/Residues: 1-29 <OLI>
A/Cross-references: UNIPROT:P05483
C/Superfamily: omega-conotoxin
C/Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F;1-16,8-19,15-26/Disulfide bonds: #status predicted
F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 17.2%; Score 28; DB 2; Length 29;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 7 CERNVDNC--CL 17
| | | | |
Db 8 CSRGVDCCTCCL 20

```

Search completed: October 29, 2004, 08:41:21  
Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 08:11:43 ; Search time 37 Seconds  
(without alignments)  
75.413 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.\*\*

2: PIR2.\*\*

3: PIR3.\*\*

4: PIR4.\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	43	2 B26356	transforming growt
2	163	100.0	112	2 A61439	transforming growt
3	163	100.0	412	2 A39489	transforming growt
4	163	100.0	414	1 WFMKB2	transforming growt
5	163	100.0	414	1 WFMKB2	transforming growt
6	163	100.0	414	2 A31249	transforming growt
7	163	100.0	442	2 B31249	transforming growt
8	160	98.2	413	1 WFXB22	transforming growt
9	133	81.6	409	2 S01825	transforming growt
10	133	81.6	410	2 A41397	transforming growt
11	133	81.6	410	2 A55706	transforming growt
12	133	81.6	412	2 A34939	transforming growt
13	133	81.6	412	2 A36169	transforming growt
14	111	68.1	130	2 I48196	transforming growt
15	111	68.1	315	2 A40057	transforming growt
16	111	68.1	390	1 WPHU2	transforming growt
17	111	68.1	390	1 WFM52	transforming growt
18	111	68.1	390	2 A26960	transforming growt
19	111	68.1	390	2 JC4052	transforming growt
20	111	68.1	390	2 A27512	transforming growt
21	111	68.1	390	2 T46463	transforming growt
22	111	68.1	390	2 S10219	transforming growt
23	111	68.1	391	2 S01413	transforming growt
24	100	61.3	34	2 C42320	transforming growt
25	96	58.9	71	2 A40699	transforming growt
26	96	58.9	382	2 B61036	transforming growt
27	95	58.3	373	2 A41918	transforming growt
28	52	31.9	89	1 IPMTA2	bombyxin A-2 precu
29	52	31.9	89	2 S69483	bombyxin A-8 precu

30 52 31.9 89 2 S69484  
31 52 31.9 92 1 IPMTA3  
32 52 31.9 92 2 S69482  
33 52 31.9 92 2 S69482  
34 52 31.9 92 2 JQ0825  
35 52 31.9 92 2 S69477  
36 52 31.9 92 2 S69481  
37 52 31.9 92 2 S69478  
38 52 31.9 92 2 S69479  
39 52 31.9 92 2 A48322  
40 50.5 31.0 478 2 S16867  
41 49 30.1 87 2 S69490  
42 49 30.1 87 2 JQ0836  
43 48 29.4 88 2 S69489  
44 48 29.4 90 1 IPMTA1  
45 48 29.4 90 1 IPMTA2

## ALIGNMENTS

### RESULT 1

B26356

transforming growth factor beta-2 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 30-Sep-1993

C:Accession: B26356

R:Chelifeitz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.; N

Cell 48, 409-415, 1987

A:Title: The transforming growth factor-beta system, a complex pattern of cross-reactive

A:Reference number: A90890; MUID:87102890; PMID:2879635

A:Accession: B26356

A:Molecule type: protein

A:Residues: 1-43 <CHE>

C:Superfamily: inhibin

C:Keywords: growth factor

Query Match 100.0%; Score 163; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.9e-16;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 29

Db 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 29

### RESULT 2

A61439

transforming growth factor beta-2 - bovine

N:Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a

C:Species: Bos primigenius taurus (cattle)

C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C:Accession: A61439; A25485; B42320; S15389

R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.

J. Protein Chem. 10, 565-575, 1991

A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta2

A:Reference number: A61439; MUID:92189724; PMID:1799413

A:Accession: A61439

A:Molecule type: protein

A:Residues: 1-112 <JIN>

A:Cross-references: UNIPROT:P21214

A:Experimental source: milk

R:Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.

J. Biol. Chem. 262, 1946-1949, 1987

A:Title: Cartilage-inducing factor-B is a unique protein structurally and functionally re

A:Reference number: A25485; MUID:87137406; PMID:3469199

A:Accession: A25485

A:Molecule type: protein

A:Residues: 1-30 <SEY>

A:Experimental source: bone

R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.

J. Biol. Chem. 267, 2325-2328, 1992

A:Title: Purification and characterization of transforming growth factor-beta2.3 and -bet

A:Reference number: A42320; MUID:32129307; PMID:1733936

A:Accession: B42320

A:Molecule type: protein

A:Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>

A:Experimental source: Done

R:Cooper, D.A.; Buerk, R.R.

Eur. J. Biochem. 197, 353-358, 1991

A:Title: Isolation and characterization of milk growth factor, a transforming-growth-factor

A:Reference number: S15389; MUID:91224126; PMID:2026157

A:Accession: S15389

A:Molecule type: protein

A:Residues: 1-16, 'XX', 19 <COX>

A:Experimental source: milk

C:Superfamily: inhibin

C:Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match 100.0%; Score 163; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 4.6e-16;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 29

|||||

Db 1 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 29

RESULT 3

A39489

transforming growth factor beta-2 precursor - chicken

N:Alternate names: TGF-beta2

C:Species: Gallus gallus (chicken)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

C:Accession: A39489; A61018; S25849

R:Burt, D.W.; Paton, I.R.

DNA Cell Biol. 10, 723-734, 1991

A:Title: Molecular cloning and primary structure of the chicken transforming growth factor

A:Reference number: A39489; MUID:92075163; PMID:1683775

A:Accession: A39489

A:Molecule type: DNA

A:Residues: 1-412 <BUR>

A:Cross-references: UNIPROT:P30371; GB:X58071; NID:G63810; PIDN:CAA41101.1; PID:G833616;

R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.

Growth Factors 2, 123-133, 1990

A:Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming growth

A:Reference number: A61018; MUID:90253805; PMID:2340183

A:Accession: A61018

A:Molecule type: mRNA

A:Status: not compared with conceptual translation

A:Residues: 1-94, 'G', 96-244, 'L', 246-412 <JAK>

C:Genetics:

A:Insertions: 115/1; 169/3; 214/1; 251/1; 309/2; 360/3

C:Superfamily: inhibin

C:Keywords: growth factor; growth regulation; mitogen; transformation

F:1-26/Domain: signal sequence #status predicted <SIG>

F:21-300/Domain: propeptide #status predicted <PRO>

F:301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match 100.0%; Score 163; DB 2; Length 412;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 29

|||||

Db 301 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 329

RESULT 4

WFMXB2

transforming growth factor beta-2 precursor, short form - green monkey

N:Alternate names: BSC-1 cell growth inhibitor; cartilage-inducing factor B; polyargin

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 23-Mar-1990 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C:Accession: A34005

R:Hanks, S.K.; Armour, R.; Baldwin, J.H.; Maldonado, F.; Spiess, J.; Holley, R.W.

Proc. Natl. Acad. Sci. U.S.A. 85, 79-82, 1988

A:Title: Amino acid sequence of the BSC-1 cell growth inhibitor (polyargin) deduced from

A:Reference number: A34005; MUID:86124824; PMID:3277172

A:Accession: A34005

A:Molecule type: mRNA

A:Residues: 1-414 <HAN>

A:Cross-references: UNIPROT:P61811; GB:J03585; NID:G176495; PIDN:AAA3358.1; PID:G176496

A:Note: part of this sequence, including the amino end of the active peptide, confirmed by

R:Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.

DNA 7, 493-497, 1988

A:Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two differer

A:Reference number: A90960; MUID:89090808; PMID:2850146

A:Contents: annotation

A:Note: although they do not show the sequences, a clone identical yielding a sequence ic

with that in the long form of the human sequence

C:Superfamily: inhibin

C:Keywords: alternative splicing; glycoprotein; growth factor; growth regulation; homodin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-302/Domain: propeptide #status predicted <PRO>

F:303-414/Product: transforming growth factor beta-2 #status predicted <MAT>

F:72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 163; DB 1; Length 414;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 29

|||||

Db 303 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 331

RESULT 5

WFMSE2

transforming growth factor beta-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004

C:Accession: A40148

R:Miller, D.A.; Lee, A.; Pelton, R.W.; Chen, E.Y.; Moses, H.L.; Derynck, R.

Mol. Endocrinol. 3, 1108-1114, 1989

A:Title: Murine transforming growth factor-beta2 cDNA sequence and expression in adult ti

A:Reference number: A40148; MUID:90014832; PMID:2797004

A:Accession: A40148

A:Molecule type: mRNA

A:Residues: 1-414 <MTL>

A:Cross-references: UNIPROT:P27090; EMBL:X57413; NID:G54772; PIDN:CAA40672.1; PID:G54773

C:Comment: None of the three predicted glycosylation sites is in the mature protein.

C:Superfamily: inhibin

C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-302/Domain: propeptide #status predicted <PRO>

F:303-414/Product: transforming growth factor beta-2 #status predicted <MAT>

F:72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 163; DB 1; Length 414;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 29

|||||

Db 303 ALDAAYCFRNVQDNCCLRLPLIYDFKRDLG 331

RESULT 6

A31249

transforming growth factor beta-2 precursor, short form - human

N:Alternate names: glioblastoma-derived T-cell suppressor factor

C:Species: Homo sapiens (man)

C:Date: 01-Dec-1989 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C:Accession: S06216; A31249

R:de Martin, R.; Haendler, B.; Hofer-Warbinek, R.; Gaugitsch, H.; Wrann, M.; Schluesener,

EMBO J. 6, 3673-3677, 1987

A:Title: Complementary DNA for human glioblastoma-derived T cell suppressor factor, a nov

A:Reference number: S06216; MUID:8811555; PMID:3322813



A:Accession: S06216  
A:Molecule type: mRNA  
A:Residues: 1-414 <DEM>  
A:Cross-references: UNIPROT:P61812; EMBL:Y00083; NID:G31959; PIDN:CAA68279.1; PID:G31960  
R:Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.  
DNA 7, 493-497, 1988  
A:Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two different precursor - African clawed frog  
A:Reference number: A90960; MUID:89090808; PMID:2850146  
A:Accession: A31249  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 101-130 <WEB>  
C:Genetics:  
A:Gene: GDB:TGF2  
A:Cross-references: GDB:120436; OMIM:190220  
A:Map position: 1q41-1q41  
C:Superfamily: inhibin  
C:Keywords: alternative splicing; growth factor  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-302/Domain: propeptide #status predicted <PRO>  
F:303-414/Product: transforming growth factor beta-2 #status experimental <MAT>  
Query Match 100.0%; Score 163; DB 2; Length 414;  
Best Local Similarity 100.0%; Pred. No. 1.5e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAFCFRNVQDNCCLRLPIYIDFKRDLG 29  
DB 303 ALDAAFCFRNVQDNCCLRLPIYIDFKRDLG 331  
RESULT 7  
B31249  
transforming growth factor beta-2 precursor, long form - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Dec-1989 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
A:Accession: A29478; A54627; A26740; A29798; B31249  
R:Madisen, L.; Webb, N.R.; Rose, T.M.; Marquardt, H.; Ikeda, T.; Twardzik, D.; Seyedin, D.N.A. 7, 1-8, 1988  
A:Title: Transforming growth factor-beta-2: cDNA cloning and sequence analysis.  
A:Reference number: A29478; MUID:88166349; PMID:3162414  
A:Accession: A29478  
A:Molecule type: mRNA  
A:Residues: 1-442 <MAD>  
A:Cross-references: UNIPROT:P61812; GB:M19154; GB:M22045; GB:M22046; NID:G339549; PIDN:A  
A:Experimental source: adenocarcinoma  
R:Noma, T.; Glick, A.B.; Geiser, A.G.; O'Reilly, M.A.; Miller, J.; Roberts, A.B.; Sporn, Growth Factors 4, 247-255, 1991  
A:Title: Molecular cloning and structure of the human transforming growth factor-beta2 gene  
A:Reference number: A54627; MUID:92110032; PMID:1764261  
A:Accession: A54627  
A:Molecule type: DNA  
A:Residues: 1-31, 'L', 33-115 <NOM>  
A:Cross-references: GB:M87843; NID:G339565; PIDN:AAA61162.1; PID:G553792  
R:Ikeda, T.; Lioubin, M.N.; Marquardt, H.  
Biochemistry 26, 2406-2410, 1987  
A:Title: Human transforming growth factor type beta-2; production by a prostatic adenocarcinoma cell line  
A:Reference number: A26740; MUID:8721633; PMID:3475130  
A:Accession: A26740  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 331-381 <IKE>  
R:Marquardt, H.; Lioubin, M.N.; Ikeda, T.  
J. Biol. Chem. 262, 12127-12131, 1987  
A:Title: Complete amino acid sequence of human transforming growth factor type beta-2.  
A:Reference number: A29798; MUID:87308213; PMID:3476488  
A:Accession: A29798  
A:Molecule type: protein  
A:Residues: 331-442 <MAR>  
R:Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.  
DNA 7, 493-497, 1988  
A:Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two different precursor - African clawed frog  
A:Reference number: A90960; MUID:89090808; PMID:2850146

A:Accession: B31249  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 101-158 <WEB>  
C:Genetics:  
A:Gene: GDB:TGF2  
A:Cross-references: GDB:120436; OMIM:190220  
A:Map position: 1q41-1q41  
C:Superfamily: inhibin  
C:Keywords: alternative splicing; growth factor  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-330/Domain: propeptide #status predicted <PRO>  
F:331-442/Product: transforming growth factor beta-2 #status experimental <MAT>  
Query Match 100.0%; Score 163; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAFCFRNVQDNCCLRLPIYIDFKRDLG 29  
DB 331 ALDAAFCFRNVQDNCCLRLPIYIDFKRDLG 359  
RESULT 8  
B31249  
transforming growth factor beta-2 precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 12-Feb-1993 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
A:Accession: S09510; A61036  
R:Rebertus, M.L.; Bhatia-Dey, N.; Dawid, I.B.  
Nucleic Acids Res. 18, 2185, 1990  
A:Title: The sequence of TGF-beta2 from Xenopus laevis.  
A:Reference number: S09510; MUID:90245678; PMID:2336403  
A:Accession: S09510  
A:Molecule type: mRNA  
A:Residues: 1-413 <REB>  
A:Cross-references: UNIPROT:P17247; EMBL:X51817; NID:G414789; PIDN:CAA361116.1; PID:G6513;  
R:Rebertus, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebertus, M.L.; Konde Growth Factors 2, 135-147, 1990  
A:Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium conditioned by 3T3-L1 cells  
A:Reference number: A61036; MUID:90253806; PMID:2340184  
A:Accession: A61036  
A:Molecule type: protein  
A:Residues: 302-307, 'X', 309-315, 'XX', 318-319 <ROB>  
C:Superfamily: inhibin  
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen  
F:1-19/Domain: signal sequence #status predicted <Sig>  
F:20-301/Domain: propeptide #status predicted <PRO>  
F:302-413/Product: transforming growth factor beta-2 #status predicted <MAT>  
F:72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 98.2%; Score 160; DB 1; Length 413;  
Best Local Similarity 96.6%; Pred. No. 4e-15;  
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAFCFRNVQDNCCLRLPIYIDFKRDLG 29  
DB 302 ALDAAFCFRNVQDNCCLRLPIYIDFKDLG 330  
RESULT 9  
S01825  
transforming growth factor beta-3 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
A:Accession: S01825  
R:Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.; Masc EMBO J. 7, 3737-3743, 1988  
A:Title: A new type of transforming growth factor-beta, TGF-beta3.  
A:Reference number: S01824; MUID:89091120; PMID:3208746  
A:Accession: S01825  
A:Molecule type: mRNA  
A:Residues: 1-409 <DER>

A;Accession: A55706  
A:Molecule type: mRNA  
A:Residues: 1-410 <WAN>  
A;Cross-references: UNIPROT:Q07258; GB:U03491  
A;Note: it is uncertain whether Met-1 is the initiator  
R;McKinnon, R.D.; Piras, G.; Ida Jr., J.A.; Dubois-Dalcq, M.  
J. Cell Biol. 121, 1397-1407, 1993  
A;Title: A role for TGF-beta in oligodendrocyte differentiation.  
A;Reference number: A40699; MUID:93286190; PMID:8509457  
A;Accession: B40699  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 157-211 <CKX>  
A;Cross-references: EMBL:X71903; NID:g311326; PIDN:CAA50722.1; PID:g311327  
C;Superfamily: inhibin

Query Match 81.6%; Score 133; DB 2; Length 410;  
Best Local Similarity 72.4%; Pred. NO. 2.8e-11;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDAYCFRNVDNCCLRLPLXYIDPKRDLG 29  
||| |||||:::|||:::|||:::|||  
Db 299 AUDTYCFRNLEENCVRPLXYIDFRQDLG 327

RESULT 12  
A34939  
Transforming growth factor beta-3 precursor - chicken  
C;Species: Gallus gallus (chicken)  
C>Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text\_change 09-Jul-2004  
C;Accession: A34939; S25850; S36125; S36124; I51181  
R;Jakowlew, S.B.; Dillard, P.J.; Kondaiah, P.; Sporn, M.B.; Roberts, A.B.  
Mol. Endocrinol. 2, 747-755, 1988  
A;Title: Complementary deoxyribonucleic acid cloning of a novel transforming growth factor  
A;Reference number: A34939; MUID:89096966; PMID:3211158  
A;Accession: A34939  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-412 <JAK>  
A;Cross-references: UNIPROT:P16047; GB:M31154; NID:g212758; PIDN:AAA49089.1; PID:g212759  
R;Burt, D.W.; Paton, I.R.; Day, B.R.  
J. Mol. Endocrinol. 7, 175-183, 1991  
A;Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and  
A;Reference number: S25850; MUID:92134496; PMID:1840616  
A;Accession: S25850  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <BUP>  
A;Cross-references: EMBL:X58127; NID:g63815; PIDN:CAA41128.1; PID:g63816  
A;Accession: S36125  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 119-172 <BU2>  
A;Cross-references: EMBL:X60055; NID:g396688; PIDN:CAA42653.1; PID:g396689  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Accession: S36124  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 173-322, 'ELPT', 327-412 <BU3>  
A;Cross-references: EMBL:X60091  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
R;Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.; Cubert, J.  
Mol. Endocrinol. 6, 1285-1298, 1992  
A;Title: Identification and characterization of the chicken transforming growth factor-beta-3  
A;Reference number: I51181; MUID:93024487; PMID:1406706  
A;Accession: I51181  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <JAZ>  
A;Cross-references: GB:S46000; NID:g257172; PIDN:AAB23575.1; PID:g257173  
C;Genetics:  
A;Introns: 216/1; 252/1; 309/2; 360/3  
A;Note: list of introns may be incomplete

C; Superfamily: Glycoprotein  
C; Keywords: glycoprotein; growth factor; heterodimer  
F; 204-315/Product: transforming growth factor beta-1 #status experimental  
F; 7,61,101/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 68.1%; Score 111; DB 2: Length 315;  
Best Local Similarity 62.1%; Pred. No. 2.9e-08;

Matches 18; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRPYIIDFKRDLG 29

Db 204 ALDTNYCFSSTEXNCCVRQLYIDFRKDLG 232

Search completed: October 29, 2004, 08:31:08  
Job time : 37 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2004, 08:40:47 ; Search time 126 Seconds  
(without alignments)  
74.621 Million cell updates/sec

Title: US-09-822-873-1  
Perfect score: 163  
Sequence: 1 ALDAAVCFRNVQNCCLRPYIDFKRDIG 29

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues  
Total number of hits satisfying chosen parameters: 313726

Minimum DB seq length: 0  
Maximum DB seq length: 29

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/FCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/FCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	29	9	US-09-822-873-1
2	163	100.0	29	14	US-10-240-421-1
3	93	57.1	20	9	US-09-822-873-5
4	93	57.1	20	14	US-10-240-421-4
5	87	53.4	16	15	US-10-430-685-31
6	78	47.9	16	9	US-09-822-873-2
7	70	42.9	16	15	US-10-430-685-29
8	61	37.4	16	9	US-09-822-873-4
9	57	35.0	16	14	US-09-822-873-7
10	57	35.0	16	14	US-10-240-421-5
11	55	33.7	16	14	US-10-240-421-3
12	52	31.9	16	9	US-09-822-873-6
13	52	31.9	16	14	US-10-240-421-5

14	50	30.7	15	14	US-10-350-405-212	Sequence 212, Appl
15	49	30.1	9	9	US-09-748-038B-28	Sequence 28, Appl
16	47	28.8	20	14	US-10-339-740-226	Sequence 226, App
17	44	27.0	16	9	US-09-822-873-3	Sequence 3, Appli
18	44	27.0	16	14	US-10-240-421-2	Sequence 2, Appli
19	44	27.0	17	14	US-10-074-152-6	Sequence 6, Appli
20	41	25.2	13	15	US-10-390-585-27	Sequence 27, Appl
21	40.5	24.8	26	10	US-09-910-082A-383	Sequence 383, App
22	40.5	24.8	26	16	US-10-765-926-383	Sequence 383, App
23	40	24.5	11	15	US-10-430-685-16	Sequence 16, Appl
24	40	24.5	23	10	US-09-214-592-1	Sequence 1, Appli
25	39	23.9	29	14	US-10-218-876-8	Sequence 8, Appli
26	38	23.3	11	15	US-10-609-217-107	Sequence 107, App
27	38	23.3	11	15	US-10-632-388-107	Sequence 107, App
28	38	23.3	11	15	US-10-651-723-107	Sequence 107, App
29	38	23.3	11	15	US-10-645-761-107	Sequence 107, App
30	38	23.3	11	15	US-10-666-696-107	Sequence 107, App
31	38	23.3	11	15	US-10-653-048-107	Sequence 107, App
32	38	23.3	26	9	US-09-864-761-41574	Sequence 41574, A
33	37.5	23.0	27	14	US-10-352-254-16	Sequence 16, Appl
34	37.5	23.0	27	14	US-10-352-254-25	Sequence 25, Appl
35	37.5	23.0	27	15	US-10-627-685-16	Sequence 16, Appl
36	37.5	23.0	27	15	US-10-627-685-25	Sequence 25, Appl
37	37	22.7	11	15	US-10-430-685-18	Sequence 18, Appl
38	36.5	22.4	27	14	US-10-352-254-18	Sequence 18, Appl
39	36.5	22.4	27	15	US-10-627-685-18	Sequence 18, Appl
40	36.5	22.4	29	14	US-10-029-386-32828	Sequence 32828, A
41	36	22.1	11	15	US-10-430-685-37	Sequence 37, Appl
42	36	22.1	15	9	US-09-759-143-804	Sequence 804, App
43	36	22.1	15	9	US-09-759-143-805	Sequence 805, App
44	36	22.1	15	9	US-09-780-669-804	Sequence 804, App
45	36	22.1	15	9	US-09-780-669-805	Sequence 805, App

ALIGNMENTS

RESULT 1  
US-09-822-873-1  
; Sequence 1, Application US/09822873  
; Patent No. US20020160012A1  
; GENERAL INFORMATION:  
; APPLICANT: KAASTRUP, Peter  
; TITLE OF INVENTION: VACCINE CHIP TECHNOLOGY EXPLOITING IMMUNO-STIMULATING FRAGMENT O  
; FILE REFERENCE: KAASTRUP-1A  
; CURRENT APPLICATION NUMBER: US/09/822, 873  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/246, 973  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: DK PA2000 00540  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-822-873-1

Query Match 100.0%; Score 163; DB 9; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.8e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAVCFRNVQNCCLRPYIDFKRDIG 29  
Db 1 ALDAAVCFRNVQNCCLRPYIDFKRDIG 29

RESULT 2  
US-10-240-421-1  
; Sequence 1, Application US/10240421  
; Publication No. US20030190322A1



Db 1 CLRPLYIDFKRDLG 14

RESULT 7

US-10-430-685-29

; Sequence 29, Application US/10430685

; Publication No. US20040039543A1

; GENERAL INFORMATION:

; APPLICANT: KECK, Peter

; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS

; FILE REFERENCE: 63040-010210

; CURRENT APPLICATION NUMBER: US/10/430,685

; CURRENT FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: PCT/US01/44000

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: 60/246,196

; PRIOR FILING DATE: 2000-11-06

; NUMBER OF SEQ ID NOS: 240

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 29

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-430-685-29

Query Match 42.9%; Score 70; DB 15; Length 16;

Best Local Similarity 73.3%; Pred. No. 0.0074;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 15 CCURPLYIDFKRDLG 29

Db 1 CCVRQLYIDFKRDLG 15

RESULT 8

US-09-822-873-4

; Sequence 4, Application US/09822873

; Patent No. US20020160012A1

; GENERAL INFORMATION:

; APPLICANT: KAASTRUP, Peter

; TITLE OF INVENTION: VACCINE CHIP TECHNOLOGY EXPLOITING IMMUNO-STIMULATING FRAGMENT OF

; FILE REFERENCE: KAASTRUP-1A

; CURRENT APPLICATION NUMBER: US/09/822,873

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: US 60/246,973

; PRIOR FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: DK PA2000 00540

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: TGF-beta fragment

US-09-822-873-4

Query Match 37.4%; Score 61; DB 9; Length 16;

Best Local Similarity 71.4%; Pred. No. 0.13;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 CLRPLYIDFKRDLG 29

Db 1 CVRQLYIDFKRDLG 14

RESULT 9

US-09-822-873-7

; Sequence 7, Application US/09822873

; Patent No. US20020160012A1

; GENERAL INFORMATION:

; APPLICANT: KAASTRUP, Peter

; TITLE OF INVENTION: VACCINE CHIP TECHNOLOGY EXPLOITING IMMUNO-STIMULATING FRAGMENT OF

; FILE REFERENCE: KAASTRUP-1A

; CURRENT APPLICATION NUMBER: US/09/822,873

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: US 60/246,973

; PRIOR FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: DK PA2000 00540

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Analogue of TGF-beta fragment

; NAME/KEY: misc\_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: Xaa is Pro or Gln

; NAME/KEY: misc\_feature

; LOCATION: (11)..(11)

; OTHER INFORMATION: Xaa is Lys or Gln

US-09-822-873-7

Query Match 35.0%; Score 57; DB 9; Length 16;

Best Local Similarity 71.4%; Pred. No. 0.46;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 16 CLRPLYIDFKRDLG 29

Db 1 CVRXYIDFKRDLG 14

RESULT 10

US-10-240-421-6

; Sequence 6, Application US/10240421

; Publication No. US20030190322A1

; GENERAL INFORMATION:

; APPLICANT: KAASTRUP, Peter

; TITLE OF INVENTION: IMMUNOSTIMULATING PROPERTIES OF A FRAGMENT OF TGF-BETA

; FILE REFERENCE: KAASTRUP-2

; CURRENT APPLICATION NUMBER: US/10/240,421

; CURRENT FILING DATE: 2002-09-30

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Mutant of fragment of TGF beta

; NAME/KEY: misc\_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: X is Pro or Gln

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (11)..(11)

; OTHER INFORMATION: X is Lys or Gln

US-10-240-421-6

Query Match 35.0%; Score 57; DB 14; Length 16;

Best Local Similarity 71.4%; Pred. No. 0.46;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 16 CLRPLYIDFKRDLG 29

Db 1 CVRXYIDFKRDLG 14

RESULT 11

US-10-240-421-3  
 ; Sequence 3, Application US/10240421  
 ; Publication No. US20030190322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAASTRUP, Peter  
 ; TITLE OF INVENTION: IMMUNOSTIMULATING PROPERTIES OF A FRAGMENT OF TGF-BETA  
 ; FILE REFERENCE: KAASTRUP-2  
 ; CURRENT APPLICATION NUMBER: US/10/240,421  
 ; CURRENT FILING DATE: 2002-09-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 3  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-240-421-3

Query Match 33.7%; Score 55; DB 14; Length 16;  
 Best Local Similarity 54.3%; Pred. No. 0.88;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 CLRPLYIDFKRDGLG 29  
 | : | | | | | : |  
 Db 1 CVRQLYIDFKDKG 14

RESULT 12  
 US-09-822-873-6  
 ; Sequence 6, Application US/09822873  
 ; Patent No. US20020160012A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAASTRUP, Peter  
 ; TITLE OF INVENTION: VACCINE CHIP TECHNOLOGY EXPLOITING IMMUNO-STIMULATING FRAGMENT OF  
 ; FILE REFERENCE: KAASTRUP-1A  
 ; CURRENT APPLICATION NUMBER: US/09/822,873  
 ; CURRENT FILING DATE: 2001-04-02  
 ; PRIOR APPLICATION NUMBER: US 60/246,973  
 ; PRIOR FILING DATE: 2000-11-13  
 ; PRIOR APPLICATION NUMBER: DK PA2000 00540  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Analogue of TGF-beta fragment  
 ; NAME/KEY: (2)..(2)  
 ; LOCATION: (2)..(2)  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (4)..(4)  
 ; OTHER INFORMATION: Xaa is Val or Leu  
 ; NAME/KEY: (10)..(10)  
 ; LOCATION: (10)..(10)  
 ; OTHER INFORMATION: Xaa is Arg or Lys  
 ; NAME/KEY: (11)..(11)  
 ; LOCATION: (11)..(11)  
 ; OTHER INFORMATION: Xaa is Lys or Gln  
 ; OTHER INFORMATION: Xaa is Lys or Gln

Query Match 31.9%; Score 52; DB 9; Length 16;  
 Best Local Similarity 71.4%; Pred. No. 2.3;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 16 CLRPLYIDFKRDGLG 29  
 | : | | | | | : |  
 Db 1 CXRXLYIDFXDGLG 14

RESULT 13

US-10-240-421-5  
 ; Sequence 5, Application US/10240421  
 ; Publication No. US20030190322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAASTRUP, Peter  
 ; TITLE OF INVENTION: IMMUNOSTIMULATING PROPERTIES OF A FRAGMENT OF TGF-BETA  
 ; FILE REFERENCE: KAASTRUP-2  
 ; CURRENT APPLICATION NUMBER: US/10/240,421  
 ; CURRENT FILING DATE: 2002-09-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Genomic sequence for the mutated fragment of TGF-beta  
 ; NAME/KEY: (2)..(2)  
 ; LOCATION: (2)..(2)  
 ; OTHER INFORMATION: X is Val or Leu  
 ; NAME/KEY: (4)..(4)  
 ; LOCATION: (4)..(4)  
 ; OTHER INFORMATION: X is Pro or Gln  
 ; NAME/KEY: (10)..(10)  
 ; LOCATION: (10)..(10)  
 ; OTHER INFORMATION: X is Arg or Lys  
 ; NAME/KEY: (11)..(11)  
 ; LOCATION: (11)..(11)  
 ; OTHER INFORMATION: X is Lys, Arg, or Gln  
 US-10-240-421-5

Query Match 31.9%; Score 52; DB 14; Length 16;  
 Best Local Similarity 71.4%; Pred. No. 2.3;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 16 CLRPLYIDFKRDGLG 29  
 | : | | | | | : |  
 Db 1 CXRXLYIDFXDGLG 14

RESULT 14  
 US-10-350-405-212  
 ; Sequence 212, Application US/10350405  
 ; Publication No. US20030215894A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Niran, Henry L.  
 ; TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors  
 ; FILE REFERENCE: to Protein Ligands  
 ; FILE REFERENCE: TSRI 35.5 CON 7/LIG  
 ; CURRENT APPLICATION NUMBER: US/10/350,405  
 ; CURRENT FILING DATE: 2003-01-24  
 ; PRIOR APPLICATION NUMBER: 09/427,576  
 ; PRIOR FILING DATE: 1999-10-26  
 ; PRIOR APPLICATION NUMBER: 08/461,583  
 ; PRIOR FILING DATE: 1995-06-02  
 ; PRIOR APPLICATION NUMBER: 08/294,879  
 ; PRIOR FILING DATE: 1994-08-23  
 ; PRIOR APPLICATION NUMBER: 08/054,864  
 ; PRIOR FILING DATE: 1993-04-28  
 ; PRIOR APPLICATION NUMBER: 07/900,502  
 ; PRIOR FILING DATE: 1992-06-16  
 ; PRIOR APPLICATION NUMBER: 07/780,415  
 ; PRIOR FILING DATE: 1991-10-22  
 ; NUMBER OF SEQ ID NOS: 227  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 212  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: retrovirus



US-10-350-405-212

Query Match 30.7%; Score 50; DB 14; Length 15;  
Best Local Similarity 53.3%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ALDAAACFRNVQDNC 15  
||| ||| : ||  
Db 1 ALDNYCFSSTKNC 15

RESULT 15

US-09-748-038B-28  
; Sequence 28, Application US/09748038B  
; Publication No. US20020040004A1  
; GENERAL INFORMATION:  
; APPLICANT: Benedict, James J.  
; APPLICANT: Ranieri, John P.  
; APPLICANT: Whitney, Marsha L.  
; APPLICANT: Akella, Rama  
; TITLE OF INVENTION: METHOD OF PROMOTING NATURAL BYPASS  
; FILE REFERENCE: SBI-042-CIP  
; CURRENT APPLICATION NUMBER: US/09/748,038B  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 09/173,989  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Bos Taurus  
US-09-748-038B-28

Query Match 30.1%; Score 49; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAACFR 9  
||| ||| |||  
Db 1 ALDAAACFR 9

Search completed: October 29, 2004, 08:52:21  
Job time : 128 secs

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 31, 2004, 14:15:38 ; Search time 60 Seconds  
(without alignments)  
173.386 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAVCFNVDNCLRLPYIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Genesecp 23Sep04: \*  
1: Genesecp1980s: \*  
2: Genesecp1990s: \*  
3: Genesecp2000s: \*  
4: Genesecp2001s: \*  
5: Genesecp2002s: \*  
6: Genesecp2003as: \*  
7: Genesecp2003bs: \*  
8: Genesecp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	100.0	29	4	AAG78516 Immunosti
2	163	100.0	30	1	AAP81600 N-termina
3	163	100.0	30	1	AAP90112 N-terminu
4	163	100.0	30	2	AAR08144 Human car
5	163	100.0	30	2	AAR22972 Cartilage
6	163	100.0	60	4	AAB68686 Human TGF
7	163	100.0	112	1	AAP80462 Sequence
8	163	100.0	112	2	AAR12403 Transform
9	163	100.0	112	2	AAR39643 Transform
10	163	100.0	112	2	AAR39644 Transform
11	163	100.0	112	2	AAR39639 Mature hu
12	163	100.0	112	2	AAR92776 Hybrid TG
13	163	100.0	112	2	AAR92774 Human TGF
14	163	100.0	112	2	AAR91960 Human TGF
15	163	100.0	112	2	AAR91957 Human tra
16	163	100.0	112	2	AAR08174 TGF activ
17	163	100.0	112	2	AAR97092 The matur
18	163	100.0	112	2	AAR08300 Human gro
19	163	100.0	112	2	AAR4208 Transform
20	163	100.0	112	3	AAR92011 Human tra
21	163	100.0	112	4	AAB35938 TGF-beta
22	163	100.0	112	5	AAM51940 Human TGF
23	163	100.0	112	6	ABU08657 Human tra
24	163	100.0	112	8	ADH11599 Human bon
25	163	100.0	112	8	ABM79531 Human tra

26	163	100.0	115	4	AAB73205 TGF-beta2
27	163	100.0	115	6	ABG76034 Human TGF
28	163	100.0	387	6	ABU52611 Human NOV
29	163	100.0	390	2	AAR20126 Sequence
30	163	100.0	413	5	AAR77102 Human tra
31	163	100.0	414	2	AAR83055 Transform
32	163	100.0	414	2	AAR73597 Human TGF
33	163	100.0	414	5	ABJ05593 Breast ca
34	163	100.0	414	8	ADJ76133 Marker ge
35	163	100.0	414	8	ADJ75306 Marker ge
36	163	100.0	427	8	ADQ17020 Murine TG
37	163	100.0	431	8	ADQ17022 Murine TG
38	163	100.0	442	1	AAP51899 Sequence
39	163	100.0	442	2	AAR05748 Human TGF
40	163	100.0	442	2	AAR20125 Sequence
41	163	100.0	442	2	AAR79922 Human tra
42	163	100.0	442	8	ADH11591 Human bon
43	160	98.2	30	1	AAP71243 Partial N
44	160	98.2	30	1	AAP80081 N-termina
45	160	98.2	30	2	AAR14285 Cartilage

ALIGNMENTS

RESULT 1  
AAG78516  
ID AAG78516 standard; peptide; 29 AA.  
XX AAG78516;  
XX AC  
XX 22-JAN-2002 (first entry)  
XX DE Immunostimulating N-terminal TGF-beta fragment.  
XX KW TGF-beta; Transforming growth factor-beta; Immunostimulating; Vaccine;  
XX KW Antibody; Cytokine; Immunise.  
XX OS Homo sapiens.  
XX PN WO200172331-A1.  
XX PD 04-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-DK000218.  
XX PR 31-MAR-2000; 2000DK-00000540.  
XX PR 13-NOV-2000; 2000US-0246973P.  
XX (VACC-) VACCINE CHIP TECHNOLOGY APS.  
XX Kaastrup P;  
XX WPI; 2001-639205/73.

A composition containing a fragment of transforming growth factor-beta with an immunogenic determinant provides increased immunogenicity of the determinant and is useful as a vaccine.

Claim 2; Page 68; 88pp; English.

The invention relates to an immunogenic composition comprising a fragment of transforming growth factor-beta (TGF-beta) capable of eliciting an immunostimulating effect, and an immunogenic determinant against which the immunogenic response is required. It is believed that when an individual is immunised with a composition comprising the TGF-beta fragment of the invention, antibodies against the fragment are generated. Following immunisation, these antibodies may also bind to naturally occurring immunosuppressing cytokines of the immunised individual. This may then result in the blocking and/or reduction of the of the inhibitory effect of naturally occurring cytokines on the immune system. The TGF-beta fragments of the invention have immunostimulant activity, and as a result may be of use in the manufacture of a medicament for enhancing the

CC immunostimulating effects of an immunisation. The current sequence  
 CC represents the immunostimulating N-terminal TGF-beta fragment  
 XX  
 SQ Sequence 29 AA;  
 Query Match 100.0%; Score 163; DB 4; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 8e-15; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 0;  
 QY 1 ALDAAYCFNRVQDNCCLRLPLIDFKRDGLG 29  
 DB 1 ALDAAYCFNRVQDNCCLRLPLIDFKRDGLG 29

RESULT 2  
 AAP81600  
 ID AAP81600 standard; protein; 30 AA.  
 XX  
 AC AAP81600;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-MAR-2003 (revised)  
 DT 14-SEP-1990 (first entry)  
 XX  
 DE N-terminal sequence of the chains of a dimeric polypeptide co-factor for  
 DE inducing cartilage formation.  
 XX  
 KW Dimeric polypeptide; cartilage/bone formation inducing co-factor;  
 KW osteoporosis treatment; connective tissue deposition;  
 KW beta-type transforming growth factor (TGF-beta); cellular proliferation.  
 XX  
 OS Mammalia.  
 XX  
 PN US4774322-A.  
 XX  
 PD 27-SEP-1988.  
 XX  
 PF 10-DEC-1987; 87US-00129864.  
 XX  
 PR 16-JUL-1984; 84US-00630938.  
 PR 08-JUL-1985; 85EP-00304848.  
 PR 19-AUG-1985; 85US-00767144.  
 PR 10-DEC-1987; 87US-00131209.  
 PR 08-JUN-1988; 88US-00204173.  
 XX  
 PA (CLGE ) COLLAGEN CORP.  
 XX  
 PI Seyedin S, Thmoas T, Bentz H, Ellingswor L, Armstrong R;  
 XX  
 WPI; 1988-292489/41.  
 XX  
 DR New polypeptide co-factor - for inducing cartilage formation and  
 PT promoting connective tissue deposition and cell proliferation, isolated  
 PT from mammalian bone.  
 XX  
 PS Claim 1(d); Page 12; 15pp; English.  
 XX  
 CC The polypeptide is found in mammalian bone, is active in beta-type  
 CC transforming growth factor (TGF-beta) assay, and is a dimer of m.w. about  
 CC 26000 (by SDS-PAGE). The polypeptide can be used (opt. together with co-  
 CC factors) to induce cartilage/bone formation (e.g. for repair,  
 CC replacement, etc. or in treatment of osteoporosis); to promote connective  
 CC tissue deposition (in absence of any activator or co-factor) and to  
 CC promote cellular proliferation (e.g. for burn or wound healing). It is  
 CC also active in the anchorage-independent cell growth assay to  
 CC characterise TGF-beta. The polypeptide is prep'd. as follows;  
 CC demineralised bone is extracted with a chaotropic agent to solubilise non  
 CC -fibrous proteins, then the extract gel-filtered to recover a 10000-  
 CC 45000 m.w. fraction. This is adsorbed on to carboxymethylcellulose cation  
 CC exchanger at pH 4.5-5.5 (pref. 4.8) under denaturing conditions and  
 CC eluted with an NaCl gradient. The 0.15-0.25 M NaCl eluate is purified by  
 CC reverse-phase HPLC or gel electrophoresis to separate the polypeptide  
 CC (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003

CC to correct PR field.)  
 XX  
 SQ Sequence 30 AA;  
 Query Match 100.0%; Score 163; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-15;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAYCFNRVQDNCCLRLPLIDFKRDGLG 29  
 DB 1 ALDAAYCFNRVQDNCCLRLPLIDFKRDGLG 29

RESULT 3  
 AAP90112  
 ID AAP90112 standard; peptide; 30 AA.  
 XX  
 AC AAP90112;  
 XX  
 DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 15-NOV-1989 (first entry)  
 XX  
 DE N-terminus of cartilage-inducing factor B.  
 XX  
 KW Cartilage-inducing factor B; cell proliferation;  
 KW transforming growth factor beta; bone growth promoting; bovine;  
 KW chondrogenic; wound and burn healing; tissue repair.  
 XX  
 OS Bos taurus; (Bovine).  
 XX  
 PN US4843063-A.  
 XX  
 PD 27-JUN-1989.  
 XX  
 PF 08-JUN-1988; 88US-00204173.  
 XX  
 PR 16-JUL-1984; 84US-00630938.  
 PR 08-JUL-1985; 85EP-00304848.  
 PR 19-AUG-1985; 85US-00767144.  
 PR 10-DEC-1987; 87US-00129864.  
 PR 10-DEC-1987; 87US-00131209.  
 XX  
 PA (CLGE ) COLLAGEN CORP.  
 XX  
 PI Seyedin S, Thomas T, Ellingswor L, Armstrong R;  
 XX  
 WPI; 1989-241418/33.  
 XX  
 DR Cell proliferation promotion and treatment of osteoporosis - using  
 PT compsns. contg. cartilage-inducing factors and co-factor.  
 XX  
 PS Claim 8; Page 65; 14pp; English.  
 XX  
 CC N-terminus of cartilage-inducing factor B (CIF-B). It is: isolated from  
 CC bovine bone; active in a transforming growth factor beta assay; is a co-  
 CC factor for inducing cartilage formation in vivo; is found as a dimer of  
 CC 26 kD. The CIFs (see AAP90112) have in vitro chondrogenic activity alone,  
 CC in vivo chondrogenic activity with co-factors, in vivo connective tissue  
 CC deposition activity alone and in vitro TGF-beta activity when combined  
 CC with epidermal growth factor. The patent claims a compsn. of TGF-beta and  
 CC CIF-A/B which can be used for wound and burn healing and tissue repair.  
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 30 AA;  
 Query Match 100.0%; Score 163; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-15;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAYCFNRVQDNCCLRLPLIDFKRDGLG 29

Db 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

## RESULT 4

AAR08144  
ID AAR08144 standard; protein; 30 AA.

XX AAR08144;  
AC AC

XX 25-MAR-2003 (revised)  
DT 28-FEB-1991 (first entry)

XX XX  
DE Human cartilage inducing factor homodimer chain.

XX Transforming growth factor; cartilages inducing factor; CIF;  
KW polycythemia; thrombocytosis; splenomegaly.

XX OS Homo sapiens.  
XX XX

PN US4971952-A.

XX 20-NOV-1990.

XX 27-OCT-1988; 88US-00263635.

XX 06-AUG-1985; 85US-00763337.

PR 06-MAR-1986; 86US-00836672.

XX (CLGE ) COLLAGEN CORP.

XX Bentz H, Ellingsworth L, Armstrong R;

XX WPI; 1990-368150/49.

XX Treating inflammation associated with transplants, etc. - using cartilage

PT inducing factor polypeptide homo:dimer cpd.

XX Claim 1; Col 20; 14pp; English.

XX CIFs may be useful for inhibition of acute/chronic inflammation and

CC treatment of red blood cell dysfunction associated with polycythemia,

CC thrombocytosis or splenomegaly. (Updated on 25-MAR-2003 to correct PR

CC field.)

XX XX Sequence 30 AA;

Query Match 100.0%; Score 163; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 8.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

Db 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

## RESULT 5

AAR22972  
ID AAR22972 standard; protein; 30 AA.

XX AAR22972;  
AC AC

XX 09-JAN-2003 (revised)  
DT 17-SEP-1992 (first entry)

XX XX  
DE Cartilage-inducing factor-B.

XX Cartilage-inducing factor-B; transforming growth factor-beta;

KW B cell production; anti-inflammatory; bone marrow transplantation;

KW chemotherapy; granulopoiesis.

XX Bos sp.

XX WO9204912-A.

XX 02-APR-1992.  
PD PD

XX 20-SEP-1991; 91WO-US006850.  
PF PF

XX 21-SEP-1990; 90US-00586363.  
PR PR

XX (CELT-) CELTRIX LAB INC.  
XX PA

XX Carlino J, Singh N, Ellingsworth L;  
XX PI

XX WPI; 1992-131884/16.  
XX DR

XX Cartilage-inducing factor of human placental polypeptide - for prodn. of B-  
PT cells in peripheral blood or to induce granulopoiesis, for humoral  
PT immunity.

XX Disclosure; Page 9; 22pp; English.

XX Cartilage inducing factor-B is a transforming growth factor-beta 2. It is  
CC used to prepare medicaments to induce B cell prodn. in peripheral blood  
CC or for inducing granulopoiesis. Such medicaments are used to treat  
CC patients with depressed B cell counts or humoral immunity, eg irradiated  
CC bone marrow recipients, those receiving chemotherapy, or those with  
CC congenital B cell growth or function disorders. CIF-B is obtd. from  
CC diverse animal sources or by recombinant DNA technology. Its most common  
CC usage will be as an anti-inflammatory in humans and domestic animals  
CC such as cattle, cats and horses. (Updated on 09-JAN-2003 to add missing  
CC OS field.)

XX XX Sequence 30 AA;

Query Match 100.0%; Score 163; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 8.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

Db 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29

## RESULT 6

AAB68686

ID AAB68686 standard; protein; 60 AA.

XX AAB68686;  
AC AC

XX 03-MAY-2001 (first entry)  
DT DT

XX Human TGFbeta2 protein #1.  
XX DE

XX Human; transforming growth factor beta2; TGFbeta2; SELEX;  
KW systemic evolution of ligands by exponential enrichment.

XX OS Homo sapiens.

XX WO200109156-A1.

XX 08-FEB-2001.  
XX PD

XX 26-JUL-2000; 2000WO-US020397.  
PF PF

XX 29-JUL-1999; 99US-00363939.  
XX PR

XX (NEXS-) NEXSTAR PHARM INC.  
XX PA

XX Pagratis N, Lochrie M, Gold L;  
XX PI

XX WPI; 2001-218217/22.  
XX DR

XX New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
PT

PS Disclosure; Page 71; 178pp; English.

CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunohistochemical reagents

XX Sequence 60 AA;

Query Match 100.0%; Score 163; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.6e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 7

AAP80462  
ID AAP80462 standard; protein; 112 AA.

XX AAP80462;

XX 25-MAR-2003 (revised)  
DT 09-JAN-2003 (revised)  
DT 05-NOV-1990 (first entry)

XX Sequence from which new transforming growth factor polypeptide(s) are  
DE derived.

XX Carcinoma treatment; tumour treatment.

XX Homo sapiens.

XX EP290012-A.

XX 09-NOV-1988.

XX 04-MAY-1988; 88EP-00107174.

XX 04-MAY-1987; 87US-00046946.

XX 30-OCT-1987; 87US-00115776.

XX (ONCO ) ONCOGEN.

XX (BRIM ) BRISTOL-MYERS CO.

XX Marquardt H, Ikeda T, Lioubin MN;

XX WPI; 1988-316293/45.

XX New transforming growth factor polypeptide(s) - used for treating  
PT hormonally responsive carcinoma(s), prodn. of antibodies and in  
PT diagnosis.

XX Claim 10; Page 14; 17pp; English.

XX A substantially pure polypeptide composition having AA sequence given in  
CC AAP80462 is claimed. Also claimed is a polypeptide comprising AA sequence  
CC of at least eight AAs included in the sequence in AAP80462. The eight  
CC polypeptide (designated TGF-beta2) may be used in the treatment of  
CC hormonally responsive carcinomas. The TGF-beta2 and fragments can also be  
CC used in diagnostics. (Updated on 09-JAN-2003 to add missing OS field.)  
XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 112 AA;

Query Match 100.0%; Score 163; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 8

AAR12403  
ID AAR12403 standard; protein; 112 AA.

XX AAR12403;

XX 25-MAR-2003 (revised)

DT 29-AUG-1991 (first entry)

XX Transforming Growth Factor beta 2.

XX TGF-beta2; biologically active protein production.

XX Homo sapiens.

XX EP433225-A.

XX 19-JUN-1991.

XX 27-NOV-1990; 90EP-00810922.

XX 06-DEC-1989; 89GB-00027546.

XX (CJBA ) CIBA GEIGY AG.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERWALTUNGS GMBH.

XX WPI; 1991-180005/25.

XX N-PSDB; AAQ11994.

XX Prodn. of Transforming Growth Factor type-beta-like proteins - by  
PT subjecting denatured monomeric form to refolding conditions.

XX Example; Page 27; 35pp; English.

XX The TGF-beta2 coding sequence was isolated from the CI-215 human glioma  
CC cell line. It was incorporated into an appropriate vector to transform  
CC Saccharomyces cerevisiae or E. coli. Monomeric TGF-beta2 was purified,  
CC denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M NaCl, 5mM EDTA,  
CC 2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps. After  
CC 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10  
CC times. The conc. soln was diluted to the original vol. with 10mM HCl and  
CC conc to a final vol of 10 ml. The supernatant from centrifugation at  
CC 5000g for 30 min contained disulphide-linked dimeric TGF-beta2. (Updated  
CC on 25-MAR-2003 to correct PA field.)

XX Sequence 112 AA;

Query Match 100.0%; Score 163; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 9

AAR39643  
ID AAR39643 standard; protein; 112 AA.

XX AAR39643;

XX 25-MAR-2003 (revised)

DT 26-AUG-1993 (first entry)

XX Transforming Growth Factor-beta2(44/45)beta1 hybrid.

XX hTGF-beta1; hTGF-beta2; hybrid protein; wound healing; cancer treatment;  
 KW bone repair; growth regulation.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..44  
 FT /note= "amino acids 1-44 of hTGF-beta2"  
 FT Region 45..112  
 FT /note= "amino acids 45-112 of hTGF-beta1"  
 XX  
 XX EP542679-A1.  
 XX  
 PD 19-MAY-1993.  
 XX  
 PD /note= "amino acids 1-44 of hTGF-beta2"  
 FT Region 45..112  
 FT /note= "amino acids 45-112 of hTGF-beta1"  
 XX  
 XX EP542679-A1.  
 XX  
 PD 19-MAY-1993.  
 XX  
 PD 03-NOV-1992; 92EP-00810845.  
 XX  
 PD 11-NOV-1991; 91EP-00810870.  
 XX  
 XX (CIBA ) CIBA GEIGY AG.  
 XX  
 XX McMaster GK, Cox D, Cerletti N, Kuhla J;  
 XX WPI; 1993-161126/20.  
 XX N-PSDB; AAQ41604.  
 XX  
 XX New hybrid transforming growth factor-beta molecules - comprise portions  
 PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
 PT antiinflammatory and immunosuppressive agents etc.  
 XX  
 PS Claim 8; Page 28; 48pp; English.  
 XX  
 CC The invention covers hybrid TGF-beta molecules consisting of parts of the  
 CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
 CC and AAQ41601, respectively). The hinge points between parts derived from  
 CC different parent isoforms are pref. between amino acids 44 and 45, 56 and  
 CC 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using  
 CC these hinge points and one part each from two of the isoforms, 6 are  
 CC preferred including the hybrid TGF-beta2(44/45)beta1. The hybrid  
 CC molecules promote cell migration, inhibit the growth of A375 melanoma  
 CC cells, accelerate the healing of partial-thickness burn wounds and full-  
 CC thickness incisional wounds and increase formation of fibrous granular  
 CC tissue. See AAQ41602-041607 for the most pref. hybrids. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 112 AA;  
 Query Match 100.0%; Score 163; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
 DB 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
 RESULT 10  
 AAR39644  
 ID AAR39644 standard; protein; 112 AA.  
 XX  
 AC AAR39644;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-AUG-1993 (first entry)  
 XX  
 XX Transforming Growth Factor-beta2(44/45)beta3 hybrid.  
 DE  
 XX hTGF-beta2; hTGF-beta3; hybrid protein; wound healing; cancer treatment;  
 KW bone repair; growth regulation.  
 KW  
 XX Homo sapiens.  
 OS  
 XX

FH Key Location/Qualifiers  
 FT Region 1..44  
 FT /note= "amino acids 1-44 of hTGF-beta2"  
 FT Region 45..112  
 FT /note= "amino acids 45-112 of hTGF-beta3"  
 XX  
 XX EP542679-A1.  
 XX  
 PD 19-MAY-1993.  
 XX  
 PD 03-NOV-1992; 92EP-00810845.  
 XX  
 PD 11-NOV-1991; 91EP-00810870.  
 XX  
 XX (CIBA ) CIBA GEIGY AG.  
 XX  
 XX McMaster GK, Cox D, Cerletti N, Kuhla J;  
 XX WPI; 1993-161126/20.  
 XX N-PSDB; AAQ41605.  
 XX  
 XX New hybrid transforming growth factor-beta molecules - comprise portions  
 PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
 PT antiinflammatory and immunosuppressive agents etc.  
 XX  
 PS Claim 8; Page 29-30; 48pp; English.  
 XX  
 CC The invention covers hybrid TGF-beta molecules consisting of parts of the  
 CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
 CC and AAQ41601, respectively). The hinge points between parts derived from  
 CC different parent isoforms are pref. between amino acids 44 and 45, 56 and  
 CC 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using  
 CC these hinge points and one part each from two of the isoforms, 6 are  
 CC preferred including the hybrid TGF-beta2(44/45)beta3. The hybrid  
 CC molecules promote cell migration, inhibit the growth of A375 melanoma  
 CC cells, accelerate the healing of partial-thickness burn wounds and full-  
 CC thickness incisional wounds and increase formation of fibrous granular  
 CC tissue. See AAQ41602-041607 for the most pref. hybrids. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 112 AA;  
 Query Match 100.0%; Score 163; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
 DB 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
 RESULT 11  
 AAR39639  
 ID AAR39639 standard; protein; 112 AA.  
 XX  
 AC AAR39639;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-AUG-1993 (first entry)  
 XX  
 XX Mature human Transforming Growth Factor-beta2.  
 DE  
 XX hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair;  
 KW growth regulation.  
 KW  
 XX Homo sapiens.  
 OS  
 XX EP542679-A1.  
 XX  
 PD 19-MAY-1993.  
 XX  
 PD 03-NOV-1992; 92EP-00810845.  
 XX  
 XX

PR 11-NOV-1991; 91EP-00810870.  
XX  
XX (CIBA ) CIBA GEIGY AG.  
PA  
XX  
XX McMaster GK, Cox D, Cerletti N, Kuhla J;  
PI  
XX WPI; 1993-161126/20.  
DR  
DR N-PSDB; AAQ41600.

XX New hybrid transforming growth factor-beta molecules - comprise portions  
XX of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
XX antinflammatory and immunosuppressive agents etc.  
PT  
XX Claim 4; Page 22-23; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts of the  
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
CC and AAQ41601, respectively). The hinge points between parts derived from  
CC different parent isoforms are pref. between amino acids 44 and 45, 56 and  
CC 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell  
CC migration, inhibit the growth of A375 melanoma cells, accelerate the  
CC healing of partial-thickness burn wounds and full-thickness incisional  
CC wounds and increase formation of fibrous granular tissue. See e.g.  
CC AAQ41602-Q41607 for pref. hybrids. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX Sequence 112 AA;

Query Match 100.0%; Score 163; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred.No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCLRLPLYLIDFKRDLG 29  
DB 1 ALDAAACFRNVQDNCLRLPLYLIDFKRDLG 29

RESULT 12  
AAR92776  
ID AAR92776 standard; protein; 112 AA.  
XX  
XX AC AAR92776;  
XX  
XX 17-JUL-1996 (first entry)  
DT  
XX  
XX Hybrid TGF-beta 2-3.  
DE  
XX Transforming growth factor type beta; TGF-beta 2; TGF-beta 3;  
KW protein renaturation; protein folding.  
XX  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH 1, 33  
FT Protein /note= "amino acids 1-44 of human TGF-beta2"  
FT Protein 45..112  
FT Protein /note= "amino acids 45-112 of human TGF-beta3"  
FT  
FN WO9603433-A1.  
PN  
XX  
XX 08-FEB-1996.  
PD  
XX  
XX 12-JUL-1995; 95WO-EP002719.  
PF  
XX  
XX 25-JUL-1994; 94EP-00810439.  
PR  
XX (CIBA ) CIBA GEIGY AG.  
PA  
XX Cerletti N;  
PI  
XX WPI; 1996-117000/12.  
DR  
XX N-PSDB; AAT17238.

XX Prodn. of dimeric biologically active transforming growth factor - by  
XX refolding denatured monomer in detergent-free folding buffer contg.  
XX specific organic solvent to improve yield.  
XX Example 1B; Page 31-32; 54pp; English.

XX Non-soluble, monomeric transforming growth factor TGF-beta 2 (AAR92774)  
XX was recovered from E. coli LC 137 (DSM 5658) transformants carrying  
XX plasmid pPLMu.TGF-beta 2, which includes the coding sequence (AAT17236)  
XX for TGF-beta 2. A biologically active, dimeric form of TGF-beta 2 was  
XX obt'd. by refolding this monomer in detergent-free buffer contg. DMSO  
XX and/or DMF. Dimers of TGF-beta 1 (AAR92773) and TGF-beta 3 (AAR92772),  
XX and hybrid dimers (see also AAR92775-77), were also produced  
XX Sequence 112 AA;

Query Match 100.0%; Score 163; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred.No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCLRLPLYLIDFKRDLG 29  
DB 1 ALDAAACFRNVQDNCLRLPLYLIDFKRDLG 29

RESULT 13  
AAR92774  
ID AAR92774 standard; protein; 112 AA.  
XX  
XX AC AAR92774;  
XX  
XX 17-JUL-1996 (first entry)  
DT  
XX  
XX Human TGF-beta 2.  
DE  
XX Transforming growth factor type beta; TGF-beta 2; protein renaturation;  
KW protein folding.  
XX  
XX Homo sapiens.  
OS  
XX WO9603433-A1.  
PN  
XX  
XX 08-FEB-1996.  
PD  
XX  
XX 12-JUL-1995; 95WO-EP002719.  
PF  
XX  
XX 25-JUL-1994; 94EP-00810439.  
PR  
XX (CIBA ) CIBA GEIGY AG.  
PA  
XX Cerletti N;  
PI  
XX WPI; 1996-117000/12.  
DR  
XX N-PSDB; AAT17236.

XX Prodn. of dimeric biologically active transforming growth factor - by  
XX refolding denatured monomer in detergent-free folding buffer contg.  
XX specific organic solvent to improve yield.  
XX Example 1B; Page 31-32; 54pp; English.

XX Non-soluble, monomeric transforming growth factor TGF-beta 2 (AAR92774)  
XX was recovered from E. coli LC 137 (DSM 5658) transformants carrying  
XX plasmid pPLMu.TGF-beta 2, which includes the coding sequence (AAT17236)  
XX for TGF-beta 2. A biologically active, dimeric form of TGF-beta 2 was  
XX obt'd. by refolding this monomer in detergent-free buffer contg. DMSO  
XX and/or DMF. Dimers of TGF-beta 1 (AAR92773) and TGF-beta 3 (AAR92772),  
XX and hybrid dimers (see also AAR92775-77), were also produced  
XX Sequence 112 AA;



Query Match	100.0%;	Score 163;	DB 2;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 3.1e-14;		
Matches	29;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ALDAAYCFRNVQDNCCLRPFLYIDFKRDLG	29	
Db	1	ALDAAYCFRNVQDNCCLRPFLYIDFKRDLG	29	
RESULT 14				
AAR91960				
ID	AAR91960 standard; protein; 112 AA.			
XX				
AC	AAR91960;			
XX				
DT	10-JUN-1996 (first entry)			
XX				
DE	Human TGF-beta-like protein, TGF-beta-2-3.			
DE	Transforming growth factor beta; TGF; regulator; method; proliferation;			
KW	differentiation; wound healing; solvent.			
KW				
XX	Homo sapiens.			
XX				
XX	Key	Location/Qualifiers		
FH	Peptide	1..44		
FT		/note= "N-terminal 44 amino acids of TGF-beta-2"		
FT	Peptide	45..112		
FT		/note= "C-terminal 68 amino acids of TGF-beta-3"		
XX				
XX	WO9603432-A1.			
XX				
XX	08-FEB-1996.			
XX				
XX	12-JUL-1995;	95WO-EP002718.		
XX				
XX	25-JUL-1994;	94EP-00810438.		
XX				
XX	(CIBA ) CIBA GEIGY AG.			
XX				
XX	Cerletti N;			
XX				
XX	WPI; 1996-116999/12.			
XX				
XX	N-PSDB; AAT15466.			
XX				
XX	Prodn. of dimeric, biologically active transforming growth factor beta -			
PT	by refolding denatured monomer in buffer contg. mild detergent and			
PT	specific organic solvents to improve yields.			
XX				
PS	Claim 17; Page 43; 59pp; English.			
XX				
XX	AAR91960 is transforming growth factor (TGF) beta-like protein, TGF-beta-			
CC	2-3. TGF beta-2-3 is a hybrid of TGF-2 and TGF-3. TGF beta hybrids were			
CC	made using a new process of producing dimeric, biologically active TGF			
CC	beta-like proteins. The new process involves treating denatured TGF beta			
CC	monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or			
CC	digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide),			
CC	DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent			
CC	allows folding of the monomer such that, after dimerisation, the TGF beta			
CC	-like protein retains biological activity and remains in soluble form.			
CC	The method allows relatively high yields of biologically active TGF beta			
CC	like proteins in their native dimeric form. TGF-beta like proteins are			
CC	multifunctional regulators of cellular activity and a typical use is to			
CC	stimulate wound healing			
XX				
XX	Sequence 112 AA;			
Query Match	100.0%;	Score 163;	DB 2;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 3.1e-14;		
Matches	29;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ALDAAYCFRNVQDNCCLRPFLYIDFKRDLG	29	

DT 26-AUG-1997 (first entry)  
 XX TGF active fragment of a TGF-beta fusion protein.  
 DE Transforming growth factor-beta fusion protein; wound healing;  
 XX artificial skin; surgery recovery time.  
 KW Homo sapiens.  
 XX WO9639430-A1.  
 XX 12-DEC-1996.  
 XX 05-JUN-1996; 96WO-US008973.  
 XX 06-JUN-1995; 95US-00470837.  
 XX (HALL/) HALL F L.  
 PA (NIMN/) NIMNI M E.  
 PA (TUAN/) TUAN T.  
 PA (WULL/) WU L.  
 PA (CHEU/) CHEUNG D T.  
 XX Hall FL, Nimni ME, Tuan T, Wu L, Cheung DT;  
 XX WPI; 1997-043065/04.  
 DR N-PSDB; AAT42772.  
 XX Prepn. of transforming growth factor-beta fusion protein - useful to  
 PT reduce surgery recovery time and to prepare artificial skin.  
 PT Claim 12; Page 47-48; 59pp; English.  
 XX A novel transforming growth factor-beta (TGF-beta) fusion protein  
 CC comprises a purification tag and a TGF active fragment. The present  
 CC sequence represents a specifically claimed TGF active fragment.  
 CC Additionally, the fusion protein may comprise proteinase-sensitive linker  
 CC sites and binding domain so the protein sequence may contain some or all  
 CC of the following elements: purification tag; proteinase site; ECM binding  
 CC site; proteinase site; TGF-beta. TGF-beta promotes wound healing, and the  
 CC fusion protein can be used to reduce surgery recovery time and in the  
 CC preparation of artificial skin. The inclusion of a purification tag  
 CC facilitates purification of the fusion protein. The proteinase site is  
 CC included to permit cleavage and release of the purification tag after  
 CC purification if desired. The extracellular matrix binding site  
 CC facilitates delivery of the fusion protein to the desired site of action.  
 CC Delivery of the TGF-beta to the site to be treated reduces the amount of  
 CC TGF-beta required to be administered to be effective and reduces the  
 CC concentration of circulating TGF-beta which may result in undesirable  
 CC effects  
 XX Sequence 112 AA;  
 SQ Query Match 100.0%; Score 163; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAVCFRNVQNCCLRLPLYIDFKDGLG 29  
 DB 1 ALDAAVCFRNVQNCCLRLPLYIDFKDGLG 29  
 RESULT 17  
 ID AAW97092  
 XX AAW97092 standard; protein; 112 AA.  
 AC AAW97092;  
 XX 20-MAR-2003 (revised)  
 DT 28-APR-1999 (first entry)  
 XX The mature form of transforming growth factor-beta-2.

KW Transforming growth factor-beta-2; TGF-beta-like protein;  
 KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;  
 KW bone repair; tissue repair; bone marrow protective agent;  
 KW cardioprotection; anti-inflammatory; immunosuppressive; ulcer; bed sore.  
 XX Homo sapiens.  
 XX EP891985-A1.  
 XX 20-JAN-1999.  
 XX 27-NOV-1990; 98EP-00113487.  
 XX 06-DEC-1989; 89GB-00027546.  
 XX 27-NOV-1990; 90EP-00810922.  
 XX (NOVS ) NOVARTIS AG.  
 XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;  
 XX WPI; 1999-083520/08.  
 XX N-PSDB; AAX15246.  
 XX Producing biologically active dimeric Transforming Growth Factor-beta -  
 PT by refolding new monomeric Transforming Growth Factor-beta, useful for  
 PT treatment of wounds and cancer.  
 XX Example 1; Page 29; 32pp; English.  
 XX The present sequence represents the mature form of transforming growth  
 CC factor-beta-2. Dimeric, biologically active TGF-beta-like protein can be  
 CC produced by subjecting the denatured monomeric form to refolding  
 CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is  
 CC useful for the production of the dimeric, biologically active TGF-beta-  
 CC like protein, which is useful for the treatment of wounds (surface or  
 CC internal) and cancer in a mammal, in bone and tissue repair, as a bone  
 CC marrow protective agent, a mediator of cardioprotection, for the  
 CC production of an anti-inflammatory or immunosuppressive preparation.  
 CC Treatment is useful for animals, especially humans, and wound treatment  
 CC (e.g. ulcers, bed sores etc.) is particularly useful for the elderly.  
 CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to  
 CC correct PR field.)  
 XX Sequence 112 AA;  
 SQ Query Match 100.0%; Score 163; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAVCFRNVQNCCLRLPLYIDFKDGLG 29  
 DB 1 ALDAAVCFRNVQNCCLRLPLYIDFKDGLG 29  
 RESULT 18  
 ID AAY08300  
 XX AAY08300 standard; protein; 112 AA.  
 AC AAY08300;  
 XX 14-JUL-1999 (first entry)  
 XX Human growth factor protein fragment TGF-Beta2.  
 XX Growth factor; human; dimer; cysteine knot; cellular inclusion body;  
 KW pharmaceutical.  
 KW Homo sapiens.  
 OS DE19748734-A1.  
 XX 06-MAY-1999.  
 XX

PF 05-NOV-1997; 97DE-01048734.  
XX  
PR 05-NOV-1997; 97DE-01048734.  
XX  
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Kaerst U, Mueller C, Rinas U, Weich H, Erdmann H;  
XX  
XX WPI; 1999-278785/24.  
XX  
XX Preparing active growth factor dimers from inclusion bodies in high  
PT yield.  
PT  
XX  
XX Claim 14; Page 12; 14pp; German.  
PS  
XX This invention describes the novel preparation of biologically active  
CC dimers of recombinant human growth factors of the cysteine knot family  
CC starting from cellular inclusion bodies. Such dimers are useful in  
CC pharmaceutical compositions and the method provides yields of 31-39.7%,  
CC in examples, compared with about 10% for the conventional method (see  
CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor  
CC protein fragments used in the method of the invention  
XX  
SQ Sequence 112 AA;  
Query Match 100.0%; Score 163; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAVCFRNVDNCCLRPLVYIDFKRDIG 29  
DB 1 ALDAAVCFRNVDNCCLRPLVYIDFKRDIG 29  
RESULT 19  
AAW84208  
ID AAW84208 standard; protein; 112 AA.  
XX  
XX AAW84208;  
AC  
XX  
XX 25-MAR-1999 (first entry)  
DT  
DE Transforming growth factor beta active fragment.  
XX  
XX Proteinase site; bone morphogenetic fusion protein; bone binding site;  
XX bone morphogenetic protein; transforming growth factor beta;  
XX active fragment; wound healing; bone growth; purification tag.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9855137-A1.  
PN  
XX  
XX 10-DEC-1998.  
PD  
XX  
XX 02-JUN-1998; 98WO-US011189.  
PF  
XX  
XX 03-JUN-1997; 97US-00869452.  
PR  
XX  
XX (NIMN/) NIMNI M E.  
PA  
XX (HALL/) HALL F L.  
PA  
XX (WULL/) WU L.  
PA (HANB/) HAN B.  
PA (SHOR/) SHORS E C.  
XX  
XX Nimni ME, Hall FL, Wu L, Han B, Shors EC;  
PI  
XX  
XX WPI; 1999-059875/05.  
DR  
XX N-PSDE; AAV99376.  
DR  
XX New bone morphogenetic fusion proteins - comprising a purification tag  
XX and a bone morphogenetic active fragment, used for enhancing wound  
XX healing or bone growth.

PS Disclosure; Page 42-43; 64pp; English.  
XX  
CC The present sequence represents a transforming growth factor beta active  
CC fragment. The protein can be used in place of a bone morphogenetic active  
CC fragment to create the fusion proteins of the invention. When a bone  
CC morphogenetic active fragment is used, the fusion proteins are designated  
CC bone morphogenetic fusion proteins. The bone morphogenetic fusion protein  
CC may contain some or all of the following elements: a purification tag, a  
CC proteinase site, an ECM/bone binding site, a second proteinase site, and  
CC a bone morphogenetic protein active fragment. The bone morphogenetic  
CC fusion proteins can be used for enhancing wound healing or bone growth  
XX  
SQ Sequence 112 AA;  
Query Match 100.0%; Score 163; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAVCFRNVDNCCLRPLVYIDFKRDIG 29  
DB 1 ALDAAVCFRNVDNCCLRPLVYIDFKRDIG 29  
RESULT 20  
AAV92011  
ID AAV92011 standard; protein; 112 AA.  
XX  
XX AAV92011;  
AC  
XX  
XX 19-JUL-2000 (first entry)  
DT  
XX  
DE Human transforming growth factor beta 2 monomer.  
XX  
XX human transforming growth factor beta 2 monomer; CKGF; mutant;  
XX cysteine knot growth factor; hairpin loop; infertility.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 1..20  
FT /note= "optionally mutated to increase electrostatic  
FT interaction between beta hairpin structure and a  
FT receptor"  
FT  
FT Domain 21..40  
FT /label= beta\_hairpin\_loop\_1  
FT /note= "mutant optionally comprises one or more  
FT substitutions in these residues"  
FT Misc-difference 41..81  
FT /note= "optionally mutated to increase electrostatic  
FT interaction between beta hairpin structure and a  
FT receptor"  
FT  
FT Domain 82..102  
FT /label= beta\_hairpin\_loop\_3  
FT /note= "mutant optionally comprises one or more  
FT substitutions in these residues"  
FT Misc-difference 103..112  
FT /note= "optionally mutated to increase electrostatic  
FT interaction between beta hairpin structure and a  
FT receptor"  
XX  
XX WO200017360-A1.  
PN  
XX  
XX 30-MAR-2000.  
PD  
XX  
XX 19-MAR-1999; 99WO-US005908.  
PF  
XX  
XX 22-SEP-1998; 98WO-US019772.  
PR  
XX  
XX (UYMA-) UNIV MARYLAND BALTIMORE.  
PA  
XX  
XX Weintraub BD, Szkudlinski MW;  
PI  
XX  
XX WPI; 2000-283585/24.  
DR





CC cell growth such as liver cancer. The BMP polypeptides and  
 CC polynucleotides are also useful for regulating nutritional partitioning,  
 CC limiting weight gain, suppressing appetite, reducing fat mass, increasing  
 CC the sensitivity of a cell to insulin or increasing glucose uptake by a  
 CC cell. This sequence represents a human BMP polypeptide of the invention.

XX Sequence 112 AA;

Query Match 100.0%; Score 163; DB 8; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29  
 DB 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29

RESULT 25  
 ABM79531  
 ID ABM79531 standard; protein; 112 AA.

XX AC ABM79531;

XX DT 22-APR-2004 (first entry)

XX DE Human transforming growth factor beta2.

XX KW Human; TGF beta; transforming growth factor beta; antagonist;  
 KW cutaneous wound; burn; wound healing; vulnerary; nephrotropic;  
 KW ophthalmological; cytostatic; antiinflammatory; hepatotropic; cardiant.

XX OS Homo sapiens.

XX PN WO2003093293-A2.

XX PD 13-NOV-2003.

XX PF 15-APR-2003; 2003WO-US011437.

XX PR 29-APR-2002; 2002US-00135946.

XX PA (UYSL-) UNIV SAINT LOUIS.

XX PI Huang JS;

XX DR WPI; 2004-042374/04.

XX PT Inhibiting activity of transforming growth factor-beta useful for  
 PT treating wounds, cancer or fibrosis, comprises administering composition  
 PT comprising peptide antagonist of transforming growth factor-beta.

XX PS Disclosure; Fig 5A; Opp; English.

XX CC The present invention relates to a method of inhibiting activity of  
 CC transforming growth factor-beta (TGF-beta), which comprises administering  
 CC a composition comprising a non-naturally occurring peptide that binds to  
 CC a TGF-beta receptor, blocks the TGF-beta receptor from binding naturally  
 CC occurring TGF-beta and inhibits the activity of TGF-beta. The method can  
 CC be used for reducing scarring due to wounds, such as burns, scrapes,  
 CC puncture wounds and lacerations, promoting re-epithelialization of a  
 CC wound, reducing the deposition of an extracellular matrix protein in the  
 CC extracellular matrix and treating diseases mediated by TGF-beta activity,  
 CC particularly glomerulonephritis, macular degeneration, intimal  
 CC hyperplasia, cancer, fibrosis (e.g. scar formation, liver cirrhosis,  
 CC kidney fibrosis, cystic fibrosis, lung fibrosis or heart fibrosis) and  
 CC respiratory distress syndrome. The present sequence is the human TGF  
 CC beta2 protein

XX Sequence 112 AA;

Query Match 100.0%; Score 163; DB 8; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29  
 DB 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29

RESULT 26

AAB73205

ID AAB73205 standard; protein; 115 AA.

XX AC AAB73205;

XX DT 11-MAY-2001 (first entry)

XX DE TGF-beta2 C-terminal sequence.

XX KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;  
 KW muscular dystrophy; musculodgenerative disease; tissue repair;  
 KW muscle wasting disease; neuromuscular disorder; spinal cord injury;  
 KW traumatic injury; congestive obstructive pulmonary disease.

XX OS Unidentified.

XX PN WO200112777-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US022884.

XX PR 19-AUG-1999; 99US-00378238.

XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Lee S, Mcpherron AC;

XX DR WPI; 2001-211209/21.

XX PT New substantially purified growth differentiation factor-8 polypeptide,  
 PT useful for treating muscle wasting disease, obesity, muscular dystrophy,  
 PT neuromuscular disorder, acquired immunodeficiency syndrome and cachexia.

XX PS Example 2; Fig 3; 124pp; English.

XX CC The present invention relates to growth differentiation factor-8 (GDF-8)  
 CC coding sequences and proteins. The present sequence is a protein, which  
 CC was used in a sequence homology comparison with the GDF-8 protein  
 CC isolated in the present invention. GDF-8 is useful for treating  
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and  
 CC muscular dystrophy), musculodgenerative diseases or in tissue repair due  
 CC to trauma, obesity and disorders related to abnormal proliferation of  
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various  
 CC organ systems, particularly cells in muscle or adipose tissues and in  
 CC gene therapy for the treatment of cell proliferative or immunological  
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for  
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord  
 CC injury, traumatic injury, congestive obstructive pulmonary disease  
 CC (COPD), AIDS or cachexia

XX Sequence 115 AA;

Query Match 100.0%; Score 163; DB 4; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29  
 DB 4 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 32

RESULT 27

ABG76034

ID ABG76034 standard; protein; 115 AA.

XX ABG76034;  
 XX 30-APR-2003 (first entry)  
 XX Human TGF-beta 2 C-terminus.  
 XX GDF-5, growth differentiation factor 5; TGF-beta; human;  
 XX transforming growth factor beta; skeletal development; endometriosis;  
 XX cartilage differentiation; cell proliferative disease; uterine tumour;  
 XX bone dysplasia; spondyloepiphyseal dysplasia; achondroplasia;  
 XX dysplasia epiphysealis; metaphyseal dysostosis; hyperchondroplasia;  
 XX enchondromatosis; hypophosphatasia; osteopetrosis; hyperphosphatasia;  
 XX cranioepiphyseal dysplasia; osteogenesis imperfecta; transgenic;  
 XX idiopathic osteoporosis; Engelman's disease; TGF beta-2.  
 XX Homo sapiens.  
 XX US2002165361-A1.  
 XX 07-NOV-2002.  
 XX 12-JUN-2001; 2001US-00880708.  
 XX 12-JAN-1993; 93US-00003144.  
 XX 12-JAN-1994; 94WO-US000657.  
 XX 31-MAY-1995; 95US-00455559.  
 XX 01-SEP-1998; 98US-00145060.  
 XX (LEES/) LEE S.  
 XX (HUYNH/) HUYNH T.  
 XX Lee S, Huynh T;  
 XX WPI; 2003-255226/25.  
 XX New antibody specifically binding to a GDF-5 polypeptide, useful for  
 XX diagnosing and treating cell proliferative disorders with aberrant GDF-5  
 XX activity, such as endometriosis, uterine tumors and those involving  
 XX skeletal tissues.  
 XX Example 2; Fig 3A; 36pp; English.  
 XX The invention relates to an antibody that specifically binds to growth  
 XX differentiation factor-5 (GDF-5, a member of the TGF-beta (transforming  
 XX growth factor beta) superfamily of proteins) polypeptide appearing as  
 XX ABG76018. In order to determine the biological activity of GDF-5 in vivo,  
 XX transgenic mice were constructed that express GDF-5 ectopically. Analysis  
 XX of two independent transgenic mouse lines showed that these animals have  
 XX ectopic bone formation with evident muscle tissue. This showed that GDF-5  
 XX was capable of inducing bone formation in vivo. The antibody is useful  
 XX for the diagnosis and treatment of cell proliferative disorders  
 XX associated with aberrant GDF-5 activity, such as endometriosis, uterine  
 XX tumors, those involving skeletal tissues, endometriosis, cartilage  
 XX differentiation, cell proliferative disease, uterine tumour, bone  
 XX dysplasia, spondyloepiphyseal dysplasia, achondroplasia, dysplasia  
 XX epiphysealis, metaphyseal dysostosis, hyperchondroplasia,  
 XX enchondromatosis, hypophosphatasia, osteopetrosis, hyperphosphatasia,  
 XX cranioepiphyseal dysplasia, osteogenesis imperfecta, idiopathic  
 XX osteoporosis and Engelman's disease. The present sequence represents a  
 XX member of the TGFbeta superfamily used to determine regions of sequence  
 XX similarity for design of degenerate primers for isolation of GDF-5  
 XX Sequence 115 AA;  
 XX Query Match 100.0%; Score 163; DB 6; Length 115;  
 XX Best Local Similarity 100.0%; Pred. No. 3, 1e-14;  
 XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX 1 ALDAAVCFRNVQDNCCLRPVLYIDFKRDLG 29  
 XX 4 ALDAAVCFRNVQDNCCLRPVLYIDFKRDLG 32

RESULT 28  
 ABUS2611.  
 ID ABUS2611 standard; protein; 387 AA.  
 XX AC ABUS2611;  
 XX 04-MAR-2003 (first entry)  
 XX Human NOVX protein, NOV18.  
 XX Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy;  
 XX obesity; infectious disease; anorexia; neurodegenerative disorder;  
 XX Alzheimer's disease; Parkinson's disease; immune disorder;  
 XX haematopoietic disorder; dyslipidaemia; metabolic disturbance;  
 XX metabolic syndrome X; wasting disorder; cancer; gene therapy; SNP;  
 XX single nucleotide polymorphism.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Misc-difference 202 /note= "May be Arg as a result of a single nucleotide  
 XX polymorphism"  
 XX WO200281518-A2.  
 XX 17-OCT-2002.  
 XX 21-FEB-2002; 2002WO-US005374.  
 XX 21-FEB-2001; 2001US-0270220P.  
 XX 21-FEB-2001; 2001US-0270523P.  
 XX 23-FEB-2001; 2001US-0270797P.  
 XX 23-FEB-2001; 2001US-0270810P.  
 XX 08-MAR-2001; 2001US-0274295P.  
 XX 16-MAR-2001; 2001US-0276400P.  
 XX 16-MAR-2001; 2001US-0276677P.  
 XX 26-MAR-2001; 2001US-0278796P.  
 XX 04-APR-2001; 2001US-0281521P.  
 XX 25-APR-2001; 2001US-0286548P.  
 XX 17-MAY-2001; 2001US-0291765P.  
 XX 10-AUG-2001; 2001US-0311595P.  
 XX 13-AUG-2001; 2001US-0311980P.  
 XX 10-SEP-2001; 2001US-0318526P.  
 XX 17-SEP-2001; 2001US-0322712P.  
 XX 18-OCT-2001; 2001US-0330307P.  
 XX (CURA-) CURAGEN CORP.  
 XX Pena CEA, Shimkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA;  
 XX Vernet CAM, Malyankar UL, Guo X, Gusev VY, Casman SJ, Boldog FL;  
 XX Furtak K, Tchernev VT, Patturajan M, Gangolli EA, Padigaru M, Liu X;  
 XX Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD;  
 XX WPI; 2003-046859/04.  
 XX N-PSDB; ABX70666.  
 XX New isolated NOVX polypeptide useful for treating cardiomyopathy,  
 XX atherosclerosis, metabolic disorders, diabetes, obesity, infectious  
 XX disease, anorexia, neurodegenerative disorders, Alzheimer's disease and  
 XX cancer.  
 XX Claim 1; Page 160; 479pp; English.  
 XX The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a,  
 XX 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15,  
 XX 16a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABUS2578-ABUS2624), a  
 XX variant of NOVX, a mature form of NOVX, and a variant of the mature form  
 XX of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding  
 XX NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX  
 XX NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining  
 XX the presence or amount of NOVX or NOVX NA in a sample, and identifying an

CC agent that binds or modulates the expression or activity of NOVX. NOVX,  
 CC NOVX NA or ab is useful for treating or preventing a NOVX-associated  
 CC disorder in a subject, preferably human. Ab is useful for determining the  
 CC presence or amount of NOVX in a sample. NOVX is useful for identifying an  
 CC agent that binds to NOVX. NOVX, NOVX NA or ab is useful for treating  
 CC metabolic disorders, diabetes, cardiomyopathy, obesity, infectious  
 CC disease, anorexia, neurodegenerative disorders, Alzheimer's disease,  
 CC Parkinson's disease, immune disorders, haematopoietic disorders, and  
 CC various dyslipidaemias, metabolic disturbances associated with obesity,  
 CC the metabolic syndrome X and wasting disorders associated with chronic  
 CC diseases, various cancers, endocrine, connective tissue, blood, vascular,  
 CC skin, renal, bone, brain, muscle disorders, or bacterial, fungal,  
 CC protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening  
 CC assays, detection assays, predictive medicine, and in methods of  
 CC treatment. NOVX is useful as immunogen, to screen for potential  
 CC ant/agonist compounds, and as bait protein in a two-hybrid or three-  
 CC hybrid assay. NOVX NA is useful in gene therapy, to express NOVX,  
 CC to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX  
 CC activity. The cell is useful for producing non-human transgenic animals.  
 CC Ab is useful for isolating, and purifying NOVX and to monitor protein  
 CC levels in tissue as part of a clinical testing procedure. The present  
 CC sequence represents a NOVX protein  
 XX  
 SQ Sequence 387 AA;

Query Match 100.0%; Score 163; DB 6; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 1e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQNCCLRPYIDFKRDLG 29  
 |||||  
 DB 276 ALDAAFCFRNVQNCCLRPYIDFKRDLG 304

## RESULT 29

AAR20126  
 ID AAR20126 standard; protein; 390 AA.

AC AAR20126;

XX 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 16-APR-1992 (first entry)

XX Sequence of hybrid transforming growth factor (TGF) beta-1/beta2.

XX Hypertension therapy; hypotensive agent; blood pressure modulator.

XX Platyrrhini.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Peptide 8..21  
 FT Protein 280..391

XX WO9119513-A.

XX 26-DEC-1991.

XX 20-JUN-1990; 90US-00541221.

XX 20-JUN-1990; 90US-00541221.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Oleson FB, Comeraski CR;

XX WPI; 1992-024199/03.

DR N-PSDB; AAQ20291.

XX Use of transforming growth factor (TGF)-beta and their antagonists - for  
 PT modulating blood pressure, for treating hypertension and hypotension.  
 XX

PS Disclosure; Fig 3; 42pp; English.

XX A new method for treating hypertension comprises administering a  
 CC transforming growth factor (TGF)-beta to an individual at a dose  
 CC effective for lowering blood pressure; the TGF-beta may be e.g. mature  
 CC TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-beta1  
 CC precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-beta2  
 CC precursor, a latent TGF-beta1 complex or a latent TGF-beta2 complex.  
 CC (Updated on 25-VAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX

SQ Sequence 390 AA;

Query Match 100.0%; Score 163; DB 2; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQNCCLRPYIDFKRDLG 29  
 |||||  
 DB 279 ALDAAFCFRNVQNCCLRPYIDFKRDLG 307

## RESULT 30

AAU77102

ID AAU77102 standard; protein; 413 AA.

XX AAU77102;

XX 05-JUN-2002 (first entry)

XX Human transforming growth factor beta 2 (TGF-beta-2) polypeptide.

XX Human; transforming growth factor beta; TGF-beta; insulin production;  
 KW type I diabetes mellitus; pancreatic cell outgrowth; wound healing;  
 KW pancreatic duct tissue; ischaemia; stroke; nervous system aging;  
 KW neurological condition; neurodegenerative disease; inflammation;  
 KW nasal injury; chemical injury; traumatic injury; tumour-induced injury;  
 KW amyotrophic lateral sclerosis; spinocerebellar degeneration;  
 KW immunological disease; multiple sclerosis; TGF-beta-2.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Region 302..413  
 FT /note= "This region is specifically claimed"

XX WO200212336-A2.

XX 14-FEB-2002.

XX 09-FEB-2001; 2001WO-US0004192.

XX 09-AUG-2000; 2000US-00635368.

XX (CURI-) CURIS INC.

XX Wang M, Pang X;

XX WPI; 2002-257468/30.

XX Treating a subject with a disorder resulting from insufficient insulin  
 production, and inducing outgrowth of pancreatic cells, involves using a  
 transforming growth factor beta therapeutic.

XX Claim 4; Fig 2; 77pp; English.

XX The invention relates to treating a subject with a disorder resulting  
 CC from insufficient insulin production, involving contacting the subject  
 CC with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta  
 CC polypeptides can be used for treating a subject with a disorder resulting  
 CC from insufficient insulin production, e.g. type I diabetes mellitus, and  
 CC for inducing outgrowth of pancreatic cells associated with pancreatic  
 CC duct tissue within a subject. A composition comprising a TGF-beta protein



CC may be useful in wound healing and treatment of neurological conditions  
CC derived from acute, subacute or chronic injury to the nervous system,  
CC including traumatic injury, chemical injury, vascular injury and deficits  
CC (such as ischaemia resulting from stroke), together with  
CC infectious/inflammatory and tumour-induced injury, aging of the nervous  
CC system including Alzheimer's disease, chronic neurodegenerative diseases  
CC including Parkinson's disease, Huntington's chorea, amyotrophic lateral  
CC sclerosis, spinocerebellar degenerations and chronic immunological  
CC diseases of the nervous system or affecting the nervous system, including  
CC multiple sclerosis. This sequence represents the human TGF-beta-2 protein  
XX  
SQ Sequence 413 AA;

Query Match 100.0%; Score 163; DB 5; Length 413;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAYCFRNVDNCCRLRPLIIDFKRDLG 29  
DB 302 ALDAAYCFRNVDNCCRLRPLIIDFKRDLG 330

RESULT 31  
AAR83055  
ID AAR83055 standard; protein; 414 AA.  
XX AC AAR83055;  
XX AC AAR83055;  
DT 27-AUG-2003 (revised)  
DT 25-JUN-1996 (first entry)  
XX DE Transforming growth factor-beta 2.  
XX KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;  
KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;  
KW nitric oxide production; hypotension; inflammation; septic shock;  
KW treatment.  
XX OS Mammalia.  
XX FH Key Location/Qualifiers  
FT Protein 303..414  
FT /note="represents the mature active TGF beta-1 mol."  
XX W09526745-A1.  
XX 12-OCT-1995.  
XX 05-APR-1994; 94WO-US003705.  
XX 05-APR-1994; 94WO-US003705.  
XX (HARD ) HARVARD COLLEGE.  
XX Lee M, Perrella MA;  
XX WPI; 1995-358443/46.  
XX N-FSDB; AAT05877.  
XX Treatment of hypotension, esp. in septic shock - by administering  
XX transforming growth factor-beta e.g. to inhibit inducible nitric oxide  
XX synthase gene transcription.  
XX Disclosure; Fig 18; 52pp; English.  
XX Transforming growth factor-beta 2 (TGF-beta 2) has been found to inhibit  
XX inducible nitric oxide synthase (iNOS) gene transcription, esp. in  
XX interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at  
XX a dose which does not inhibit constitutive NOS. TGF-beta 1 (AAR83054) or 2  
XX or their active fragments (esp. derived from the carboxy-terminal 112  
XX amino acids), can be used in the treatment of hypotension, such as that  
XX associated with severe inflammation or septic shock. (Updated on 27-AUG-  
XX 2003 to correct OS field.)

XX  
SQ Sequence 414 AA;  
Query Match 100.0%; Score 163; DB 2; Length 414;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAYCFRNVDNCCRLRPLIIDFKRDLG 29  
DB 303 ALDAAYCFRNVDNCCRLRPLIIDFKRDLG 331

RESULT 32  
AAR73597  
ID AAR73597 standard; protein; 414 AA.  
XX AC AAR73597;  
XX AC AAR73597;  
DT 25-MAR-2003 (revised)  
DT 20-DEC-1995 (first entry)  
XX DE Human TGF-beta 2 protein.  
XX KW Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;  
KW TGF-beta 2; TGF-beta 3; osteogenic cell source; OCS; bone deficiency;  
KW bone-inducing cofactor.  
XX OS Homo sapiens.  
XX US5409896-A.  
XX 25-APR-1995.  
XX 12-NOV-1993; 93US-00132405.  
XX 01-SEP-1989; 89US-00401906.  
XX 12-NOV-1991; 91US-00790856.  
XX 18-MAY-1993; 93US-00063841.  
XX (GETH ) GENENTECH INC.  
XX Rudman CG, Ammann AJ;  
XX WPI; 1995-169610/22.  
XX Compens. for treating skeletal tissue deficiency - comprising transforming  
XX growth factor-beta and an osteogenic cell source in a carrier.  
XX Disclosure; Col 17-20; 19pp; English.  
XX This sequence represents human transforming growth factor-beta 2 (TGF-  
XX beta 2). The sequences for human TGF-beta 1 (see AAR73596) and human TGF-  
XX beta 3 (see AAR73598) are claimed within the scope of the invention. The  
XX invention is a composition consisting of a TGF-beta protein and an  
XX osteogenic cell source (OCS) formulated in an acceptable carrier other  
XX than a bone morphogenic cofactor. This composition can be used for the  
XX restoration of bone deficiency. This provides for the generation of a  
XX mature bone only where it is required, without the inclusion of a  
XX specific bone-inducing cofactor. This method can be used with any of the  
XX 5 human TGF-beta's or with TGF-beta from other species. (Updated on 25-  
XX MAR-2003 to correct PF field.)

Query Match 100.0%; Score 163; DB 2; Length 414;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAYCFRNVDNCCRLRPLIIDFKRDLG 29  
DB 303 ALDAAYCFRNVDNCCRLRPLIIDFKRDLG 331





CC after different clinical or experimental treatments). They are also  
 CC useful for prognosing and diagnosing disease states such as cancer, sound  
 CC healing, atherosclerosis and hereditary haemorrhagic telangiectasia, for  
 CC testing possible drug or other therapeutic treatments, or other regimens  
 CC that might (un)intentionally alter the expression level (or stability) of  
 CC a TGF-beta receptor. The sequences of the invention are also useful in  
 CC protein therapy and in gene therapy. The present sequence is murine TGF-  
 CC beta2/N+5 FLAG fusion protein. This sequence is used in the  
 CC exemplification of the invention.  
 XX Sequence 427 AA;  
 SQ

Query Match 100.0%; Score 163; DB 8; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLVDFKRDLG 29  
 Db 316 ALDAAVCFRNVDNCCLRPLVDFKRDLG 344

RESULT 37  
 ADQ17022  
 ID ADQ17022 standard; protein; 431 AA.  
 AC ADQ17022;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX Murine TGF-beta2/N+5 HA fusion protein.  
 XX Transforming growth factor-beta; TGF-beta; medical setting;  
 KW veterinary setting; cancer; immune disorder; sound healing;  
 KW atherosclerosis; hereditary haemorrhagic telangiectasia; protein therapy;  
 KW gene therapy; murine; HA; haemagglutinin.  
 XX Mus musculus.  
 OS Synthetic.  
 XX

Key Location/Qualifiers  
 FT Peptide 1..302  
 FT /label= Signal\_peptide  
 FT Protein 303..431  
 FT /note= "Murine TGF-beta2/N+5 HA mature fusion protein"  
 FT Region 303..307  
 FT /note= "Amino acid residues 1 to 5 of TGF-beta 2"  
 FT Region 308..319  
 FT /note= "HA tag peptide"  
 XX  
 XX US6756215-B1.  
 XX  
 XX 29-JUN-2004.  
 XX  
 XX 19-OCT-2001; 2001US-00017372.  
 XX  
 XX 20-OCT-2000; 2000US-0242292P.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Wolfraim LA, Letterio JJ;  
 XX  
 XX WPI; 2004-477587/45.  
 DR N-PSDB; ADQ17021.  
 XX  
 XX New functional transforming growth factor (TGF) beta family fusion  
 FT protein, useful for treating a disease that responds to administration of  
 FT a TGF-beta family protein and for prognosing and diagnosing disease  
 FT states such as cancer.  
 XX  
 XX Example 5; SEQ ID NO 27; 71pp; English.  
 PS  
 XX The invention relates to transforming growth factor-beta (TGF-beta)  
 CC family fusion proteins that display substantial native TGF-beta family

CC protein function while also having an additional functionality conveyed  
 CC by the addition of a functionalising peptide domain (e.g. tag peptide).  
 CC The fusion proteins are useful in medical and veterinary settings. They  
 CC are useful for treating a disease that responds to administration of a  
 CC TGF-beta family protein and for assessing a pharmacologic property of a  
 CC protein. The functionalised TGF-beta fusion proteins are useful for  
 CC detecting tagged ligand in transfected cells, for detecting of cell  
 CC surface expression of TGF-beta receptor complexes by flow cytometry, and  
 CC for measuring cell surface levels of receptor complexes in non-  
 CC radioactive cross-linking assays. The tagged protein are useful for  
 CC studying TGF-beta receptor expression levels in different tissues (e.g.  
 CC of patients with cancer and immune disorders) or at different times (e.g.  
 CC after different clinical or experimental treatments). They are also  
 CC useful for prognosing and diagnosing disease states such as cancer, sound  
 CC healing, atherosclerosis and hereditary haemorrhagic telangiectasia, for  
 CC testing possible drug or other therapeutic treatments, or other regimens  
 CC that might (un)intentionally alter the expression level (or stability) of  
 CC a TGF-beta receptor. The sequences of the invention are also useful in  
 CC protein therapy and in gene therapy. The present sequence is murine TGF-  
 CC beta2/N+5 HA fusion protein. This sequence is used in the exemplification  
 CC of the invention.  
 XX Sequence 431 AA;  
 SQ

Query Match 100.0%; Score 163; DB 8; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLVDFKRDLG 29  
 Db 320 ALDAAVCFRNVDNCCLRPLVDFKRDLG 348

RESULT 38  
 AAP91899  
 ID AAP91899 standard; protein; 442 AA.  
 XX AAP91899;  
 AC AAP91899;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-DEC-1990 (first entry)  
 XX  
 DE Sequence encoded by human transforming growth factor (TGF) beta-2  
 DE precursor 442 cDNA in pPC-21.  
 XX Cell differentiation; cell proliferation.  
 XX Homo sapiens.  
 OS

Key Location/Qualifiers  
 FT Peptide 4..119  
 FT /note= "Signal"  
 FT Region 20..442  
 FT /note= "Claimed"  
 FT Cleavage-site 20..21  
 FT Modified-site 72  
 FT /note= "Potential glycosylation site"  
 FT Region 116..144  
 FT /note= "this entire SQ is replaced with Asn in simian TGF  
 FT -beta-2-414"  
 FT Modified-site 168  
 FT /note= "Potential glycosylation site"  
 FT Modified-site 269  
 FT /note= "Potential glycosylation site"  
 FT Protein 331..442  
 XX DE3833897-A.  
 XX  
 XX 03-MAY-1989.  
 XX  
 XX 05-OCT-1988; 88DE-03833897.  
 XX  
 XX 06-OCT-1987; 87US-00106752.  
 PR

PR 25-JAN-1988; 88US-00148267.  
PR 18-AUG-1988; 88US-00234065.  
XX (ONCO ) ONCOGEN.  
XX  
PI Purchio A, Madisen L, Webb N;  
XX  
XX WPI; 1989-138796/19.  
DR N-PSDB; AAN90767.  
XX  
XX New DNA sequence encoding transforming growth factor beta 2 - used for  
PT large scale expression in eucaryotic cells.  
XX  
XX Claim 4; Fig 1a; 27pp; German.  
PS  
CC PolyA-RNA was isolated from the tamoxifen-treated, human prostatic  
CC adenocarcinoma line PC-3 and converted to cDNA. TGF DNA is pref. used for  
CC control of the SV40 promoter. and expressed in CHO cells. The simian SQ  
CC is also claimed. (Updated on 25-MAR-2003 to correct PR field.) (Updated  
CC on 25-MAR-2003 to correct PA field.)  
XX  
XX SQ Sequence 442 AA;  
Query Match 100.0%; Score 163; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 331 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 359  
RESULT 39  
AAR05748  
ID AAR05748 standard; protein; 442 AA.  
XX  
AC AAR05748;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-NOV-1990 (first entry)  
XX  
XX Human TGF-Beta2-442 precursor.  
XX  
XX Human TGF-Beta2 precursor; cancer; tumoricide; ss.  
XX  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 4..19  
FT /label= Sinat peptide  
FT Protein 331..442  
XX  
DN EP376785-A.  
XX  
PD 04-JUL-1990.  
XX  
XX 14-DEC-1989; 89EP-00403480.  
XX  
XX 16-DEC-1988; 88US-00285140.  
PR 05-DEC-1989; 89US-00446020.  
XX  
XX (ONCO ) ONCOGEN LP.  
XX  
XX Purchio AF, Madisen L, Webb N;  
PI  
XX  
XX WPI; 1990-203127/27.  
DR N-PSDB; AAR05126.  
XX  
XX Cloning and expression of transforming growth factor beta 2 - used for  
PT treatment of tumours or for augmenting wound healing.  
PT  
XX  
PS Claim 1; Fig 1a; 58pp; English.  
XX

CC TGF-Beta2 may be used in treatment of tumors at effective doses, and may  
CC also be useful in augmenting wound healing by stimulating cell  
CC proliferation. The growth factor can be produced at high levels from a  
CC CHO expression system. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX SQ Sequence 442 AA;  
Query Match 100.0%; Score 163; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 331 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 359  
RESULT 40  
AAR20125  
ID AAR20125 standard; protein; 442 AA.  
XX  
AC AAR20125;  
XX  
XX 25-MAR-2003 (revised)  
DT 16-APR-1992 (first entry)  
XX  
XX Sequence of human transforming growth factor (TGF) beta-2-442.  
XX  
XX Hypertension therapy; hypotensive agent; blood pressure modulator.  
XX  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 4..19  
FT Protein 330..442  
XX  
PN WO9119513-A.  
XX  
PD 26-DEC-1991.  
XX  
XX 20-JUN-1990; 90US-00541221.  
XX  
XX 20-JUN-1990; 90US-00541221.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Oleson FB, Comerdeski CR;  
XX  
XX WPI; 1992-024199/03.  
DR N-PSDB; AAQ20290.  
XX  
XX Use of transforming growth factor (TGF)-beta and their antagonists - for  
PT modulating blood pressure, for treating hypertension and hypotension.  
XX  
XX Disclosure; Fig 2; 42pp; English.  
XX  
XX A new method for treating hypertension comprises administering a  
CC transforming growth factor (TGF)-beta to an individual at a dose  
CC effective for lowering blood pressure; the TGF-beta may be e.g. mature  
CC TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-beta1  
CC precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-beta2  
CC precursor, a latent TGF-beta1 complex or a latent TGF-beta2 complex.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX SQ Sequence 442 AA;  
Query Match 100.0%; Score 163; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29  
DB 331 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 359

RESULT 41  
 AAR79922 standard; protein; 442 AA.  
 ID AAR79922 standard; protein; 442 AA.  
 AC AAR79922;  
 DT 25-MAR-2003 (revised)  
 DT 28-MAY-1996 (first entry)  
 XX  
 DE Human transforming growth factor-2.  
 XX  
 XX TGF-beta2; transforming growth factor; protein;  
 KW cell differentiation; cell proliferation; CHO; Chinese hamster; ovary;  
 KW COS; monkey kidney; animal; mammal.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 4..19  
 FT /note= "signal peptide"  
 FT Cleavage-site 20..21  
 FT /note= "putative signal sequence cleavage site"  
 FT Peptide 331..442  
 FT /note= "mature peptide"  
 XX  
 PN EP676474-A1.  
 XX  
 XX 11-OCT-1995.  
 XX  
 XX 14-DEC-1989; 95EP-00104223.  
 XX  
 PR 16-DEC-1988; 88US-00285140.  
 PR 05-DEC-1989; 89US-00446020.  
 XX  
 XX (ONCO ) ONCOGEN LP.  
 XX  
 XX Purchio AF, Madisen L, Webb N;  
 DR WPI; 1995-346094/45.  
 DR N-PSDB; AAT04116.  
 XX  
 XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used to  
 FT produce biologically active, mature TGF-beta-2.  
 XX  
 PS Disclosure; Fig 1a; 52pp; English.  
 XX  
 CC This sequence is expressed in a host cell, preferably a COS or CHO cell,  
 CC so the host cell produces active TGF-beta2. The produced TGF-beta2  
 CC protein can be used to regulate cellular differentiation and  
 CC proliferation. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 442 AA;  
 Query Match 100.0%; Score 163; DB 2; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAVCFNRVQDNCCLRPPLYIDFKEDLG 29  
 DB 331 ALDAAVCFNRVQDNCCLRPPLYIDFKEDLG 359

RESULT 42  
 ADH11591  
 ID ADH11591 standard; protein; 442 AA.  
 XX  
 AC ADH11591;  
 XX  
 DT 11-MAR-2004 (first entry)  
 DE Human bone morphogenic protein (BMP) polypeptide #17.  
 XX

KW Human; bone morphogenic protein; BMP; weight gain; appetite suppression;  
 KW fat mass reduction; cell sensitivity; glucose uptake; diabetes;  
 KW insulin resistance; hyperglycaemia; hypertension;  
 KW coronary artery disease; renal failure; neuropathy; metabolic disorder;  
 KW glucose metabolism disorder; endocrine disorder; obesity; weight loss;  
 KW liver disorder; cartilage growth disorder; bone growth disorder;  
 KW inflammation; aberrant cell growth; liver cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003224501-A1.  
 PN  
 XX 04-DEC-2003.  
 PD  
 XX 14-FEB-2003; 2003US-00366345.  
 PF  
 XX 17-MAR-2003; 2000US-0190067P.  
 PR 16-MAR-2001; 2001US-00809269.  
 PR 23-MAR-2001; 2001WO-US009229.  
 PR 17-JAN-2002; 2002US-0348621P.  
 PR 22-JAN-2002; 2002US-0349356P.  
 PR 28-JAN-2002; 2002US-0351520P.  
 PR 06-FEB-2002; 2002US-0354265P.  
 PR 15-FEB-2002; 2002US-0356749P.  
 PR 16-JAN-2003; 2003US-00345236.  
 XX  
 PA (YOUNG) YOUNG P E.  
 PA (RUBE) RUBEN S M.  
 XX  
 XX Young PE, Ruben SM;  
 PI WPI; 2004-022075/02.  
 DR N-PSDB; ADH11568.  
 XX  
 XX New bone morphogenic protein polypeptides and polynucleotides, useful for  
 PT diagnosing, preventing, treating or ameliorating a medical condition,  
 PT e.g. diabetes, dyslipidemia, hypertension, coronary artery disease or  
 PT neuropathy.  
 XX  
 PS Claim 1; SEQ ID NO 47; 224pp; English.  
 XX  
 CC The invention relates to human bone morphogenic protein (BMP)  
 CC polypeptides and the polynucleotides encoding them. The invention also  
 CC relates to a method for limiting weight gain, suppressing appetite or  
 CC reducing fat mass, comprising administering to a mammalian subject a  
 CC therapeutic amount of a BMP polypeptide, and a method for increasing the  
 CC sensitivity of a cell to insulin or increasing glucose uptake by a cell,  
 CC comprising contacting the cell with a BMP polypeptide. The BMP  
 CC polypeptides and polynucleotides are useful for diagnosing a pathological  
 CC condition or a susceptibility to a pathological condition in a subject or  
 CC for preventing, treating or ameliorating a medical condition, e.g.  
 CC diabetes, insulin resistance, hyperglycaemia, hypertension, coronary  
 CC artery disease, renal failure, neuropathy, metabolic disorders, glucose  
 CC metabolism disorder, endocrine disorders, obesity, weight loss, liver  
 CC disorders, cartilage and bone growth disorders, inflammation or aberrant  
 CC cell growth such as liver cancer, the BMP polypeptides and  
 CC polynucleotides are also useful for regulating nutritional partitioning,  
 CC limiting weight gain, suppressing appetite, reducing fat mass, increasing  
 CC the sensitivity of a cell to insulin or increasing glucose uptake by a  
 CC cell. This sequence represents a human BMP polypeptide of the invention.  
 XX  
 SQ Sequence 442 AA;  
 Query Match 100.0%; Score 163; DB 8; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALDAAVCFNRVQDNCCLRPPLYIDFKEDLG 29  
 DB 331 ALDAAVCFNRVQDNCCLRPPLYIDFKEDLG 359

Search completed: October 31, 2004, 14:28:36

Job time : 73 secs

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is Page Blank (uspio)



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2004, 14:08:37 ; Search time 25 Seconds  
(without alignments)  
76.929 Million cell updates/sec

Title: US-09-822-873-1

Perfect score: 163

Sequence: 1 ALDAAVCFRNVQDNCCLRLPLIDFKRDLG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 56318000 residues

Total number of hits satisfying chosen parameters: 46

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	60	3	US-09-363-939A-123
2	163	100.0	60	4	US-09-791-301-123
3	163	100.0	70	4	US-09-848-664A-10
4	163	100.0	112	1	US-07-979-441-2
5	163	100.0	112	1	US-08-486-057B-42
6	163	100.0	112	1	US-08-470-837-32
7	163	100.0	112	2	US-08-789-588-42
8	163	100.0	112	3	US-08-691-794-5
9	163	100.0	112	3	US-09-123-233-4
10	163	100.0	112	3	US-09-123-233-10
11	163	100.0	112	3	US-08-927-433-3
12	163	100.0	112	3	US-08-868-452-32
13	163	100.0	112	3	US-09-095-637D-2
14	163	100.0	114	1	US-08-481-377-24
15	163	100.0	114	2	US-08-491-835-22
16	163	100.0	114	3	US-09-153-733A-24
17	163	100.0	114	3	US-08-946-092A-22
18	163	100.0	114	3	US-09-172-062-22
19	163	100.0	114	3	US-08-624-635-23
20	163	100.0	114	3	US-09-301-520D-22
21	163	100.0	114	3	US-09-389-705-24
22	163	100.0	114	5	PCT-US94-00665-24
23	163	100.0	114	5	PCT-US94-00685-22
24	163	100.0	115	1	US-08-581-529B-20
25	163	100.0	115	1	US-08-455-558-26
26	163	100.0	115	2	US-08-525-596B-30
27	163	100.0	115	2	US-08-581-528A-20

28	163	100.0	115	3	US-09-097-616-20	Sequence 20, Appl
29	163	100.0	115	3	US-09-177-860A-30	Sequence 30, Appl
30	163	100.0	115	3	US-09-145-060-26	Sequence 26, Appl
31	163	100.0	115	4	US-09-378-238-40	Sequence 40, Appl
32	163	100.0	115	4	US-09-629-938-30	Sequence 30, Appl
33	163	100.0	115	4	US-09-686-344-48	Sequence 48, Appl
34	163	100.0	115	4	US-09-412-791D-20	Sequence 20, Appl
35	163	100.0	115	4	US-09-619-061-20	Sequence 20, Appl
36	163	100.0	115	5	PCT-US94-00657-26	Sequence 26, Appl
37	163	100.0	115	5	PCT-US94-07762-20	Sequence 20, Appl
38	163	100.0	115	5	PCT-US94-07799-20	Sequence 20, Appl
39	163	100.0	414	1	US-08-132-405-2	Sequence 2, Appl
40	163	100.0	414	1	US-08-395-939A-2	Sequence 2, Appl
41	163	100.0	414	5	PCT-US91-01861-2	Sequence 2, Appl
42	163	100.0	414	5	PCT-US94-03705-6	Sequence 6, Appl
43	163	100.0	414	6	5221620-4	Patent No. 5221620
44	163	100.0	427	4	US-10-017-372E-25	Sequence 25, Appl
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ALIGNMENTS

RESULT 1  
US-09-363-939A-123  
; Sequence 123, Application US/09363939A  
; Patent No. 6346611  
; GENERAL INFORMATION:  
; APPLICANT: Pagratis, Nikos  
; APPLICANT: Lochrie, Michael  
; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
; FILE REFERENCE: INHIBITORS  
; CURRENT APPLICATION NUMBER: US/09/363,939A  
; CURRENT FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: 09/046,247  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: 08/458,424  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 07/714,131  
; PRIOR FILING DATE: 1991-06-10  
; PRIOR APPLICATION NUMBER: 07/931,473  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/964,624  
; PRIOR FILING DATE: 1992-10-21  
; PRIOR APPLICATION NUMBER: 08/117,991  
; PRIOR FILING DATE: 1993-09-08  
; PRIOR APPLICATION NUMBER: 07/536,428  
; PRIOR FILING DATE: 1990-06-11  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 123  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-363-939A-123

Query Match 100.0%; Score 163; DB 3; Length 60;

Best Local Similarity 100.0%; Pred. No. 3.7e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRLPLIDFKRDLG 29

Db 1 ALDAAVCFRNVQDNCCLRLPLIDFKRDLG 29

RESULT 2

US-09-791-301-123

Sequence 123, Application US/09791301  
Patent No. 6713616  
GENERAL INFORMATION:  
APPLICANT: Pagratiss, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGF-beta Nucleic Acid Ligands and Inhibitors  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
PRIOR APPLICATION NUMBER: 09/363,939  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 123  
LENGTH: 60  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Sequence  
US-09-791-301-123

Query Match 100.0%; Score 163; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.7e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 29

RESULT 3  
US-09-848-664A-10  
Sequence 10, Application US/09848664A  
Patent No. 6723344  
GENERAL INFORMATION:  
APPLICANT: Sakiyama-Elbert, Shelly E.  
APPLICANT: Hubbell, Jeffrey A.  
TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth Factors from Heparin Containing Matrices  
FILE REFERENCE: ETH 108  
CURRENT APPLICATION NUMBER: US/09/848,664A  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: US/09/298,084A  
PRIOR FILING DATE: 1999-04-22  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 70  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-848-664A-10

Query Match 100.0%; Score 163; DB 4; Length 70;  
Best Local Similarity 100.0%; Pred. No. 4.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 29

RESULT 4  
US-07-979-441-2  
Sequence 2, Application US/07979441  
Patent No. 5462925  
GENERAL INFORMATION:  
APPLICANT: OGAWA, YASUSHI  
APPLICANT: SCHMIDT, DAVID  
APPLICANT: DASCH, JAMES  
TITLE OF INVENTION: NOVEL BETA-TYPE TRANSFORMING GROWTH FACTOR  
TITLE OF INVENTION: FACTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/979,441  
FILING DATE: 19921120  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/614,306  
FILING DATE: 16-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: CIOTTI, THOMAS E.  
REGISTRATION NUMBER: 21,013  
REFERENCE/DOCKET NUMBER: 220952024800  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-979-441-2

Query Match 100.0%; Score 163; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 29  
Db 1 ALDAAFCFRNVQDNCCLRLPLYIDFKDGLG 29

RESULT 5  
US-08-486-057B-42  
Sequence 42, Application US/08486057B  
Patent No. 5650494  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly Produced TGF-beta-like Proteins  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Henry P. No. 5650494ak  
;; STREET: 520 White Plains Road, P.O. Box 2005  
;; CITY: Tarrytown  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10591-9005  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/486,057B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION NUMBER: 514  
;; FILING DATE: 25-FEB-1994  
;; APPLICATION NUMBER: US 08/201,703  
;; FILING DATE: 03-DEC-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/960,309  
;; FILING DATE: 13-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/621,502  
;; FILING DATE: 03-DEC-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 8927546.5  
;; FILING DATE: 06-DEC-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 5650494ak, Henry P.  
;; REGISTRATION NUMBER: 33200  
;; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (908) 277-5110  
;; TELEFAX: (908) 277-4306  
;; INFORMATION FOR SEQ ID NO: 42:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 112 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-486-057B-42

Query Match 100.0%; Score 163; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCRLRPLYIDFKRDLG 29  
|||  
Db 1 ALDAAYCFRNVDNCCRLRPLYIDFKRDLG 29

RESULT 6  
US-08-470-837-32  
; Sequence 32, Application US/08470837  
; Patent No. 5800811  
; GENERAL INFORMATION:  
; APPLICANT: Nimni, Marcel E.  
; APPLICANT: Hall, Frederick L.  
; APPLICANT: Tuan, Tai-Lan  
; APPLICANT: Wu, Lingtao  
; APPLICANT: Cheung, David T.  
; TITLE OF INVENTION: Transforming Growth Factor B Fusion  
; TITLE OF INVENTION: and  
; TITLE OF INVENTION: Their Use in Wound Healing  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 11150 Santa Monica Boulevard, Suite 400  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90025-3395

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/470,837  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sharp, Janice A.  
;; REGISTRATION NUMBER: 34,051  
;; REFERENCE/DOCKET NUMBER: 30630-1US01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 310-445-1140  
;; TELEFAX: 310-445-9031  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 112 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-470-837-32

Query Match 100.0%; Score 163; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 7.1e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAYCFRNVDNCCRLRPLYIDFKRDLG 29  
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Db 1 ALDAAYCFRNVDNCCRLRPLYIDFKRDLG 29

RESULT 7  
US-08-789-588-42  
; Sequence 42, Application US/08789588  
; Patent No. 5922846  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5922846ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/789,588  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/486,057  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: US 08/201,703  
;; FILING DATE: 25-FEB-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/960,309  
;; FILING DATE: 13-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/621,502  
;; FILING DATE: 03-DEC-1990

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-691-794-5

Query Match 100.0%; Score 163; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29
DB 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 9
US-09-123-233-4
; Sequence 4, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-123-233-4

Query Match 100.0%; Score 163; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29
DB 1 ALDAAFCFRNVQDNCCLRLPLYIDFKRDLG 29

RESULT 10
US-09-123-233-10
; Sequence 10, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-123-233-10

Query Match      100.0%; Score 163; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
   |||||
Db 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29

RESULT 11
US-08-927-433-3
; Sequence 3, Application US/08927433
; Patent No. 6107476
; GENERAL INFORMATION:
; APPLICANT: Brlander, Mark G.
; APPLICANT: Huang, Shaoming
; APPLICANT: Jackson, Michael A.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND RELATED
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One J & J Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,433
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrison, Alan J.
; REGISTRATION NUMBER: 37,399
; REFERENCE/DOCKET NUMBER: ORT-849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-3592
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-927-433-3

Query Match      100.0%; Score 163; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
   |||||
Db 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29

RESULT 12
US-08-868-452-32
; Sequence 32, Application US/08868452C
; Patent No. 6352972
; GENERAL INFORMATION:
; APPLICANT: Marcel E. Nimmi
; APPLICANT: Frederick L. Hall
```

```
; APPLICANT: Lingtao Wu
; APPLICANT: Bo Han
; APPLICANT: Edwin Shors
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS AND THEIR
; FILE REFERENCE: 17972-11
; CURRENT APPLICATION NUMBER: US/08/868,452C
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-08-868-452-32

Query Match      100.0%; Score 163; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
   |||||
Db 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29

RESULT 13
US-09-095-637D-2
; Sequence 2, Application US/09095637D
; Patent No. 6500920
; GENERAL INFORMATION:
; APPLICANT: HUANG, Jung S.
; TITLE OF INVENTION: AN INHIBITOR OF TRANSFORMING GROWTH FACTOR BETA AND A
; TITLE OF INVENTION: METHOD OF INHIBITING THE BIOLOGICAL EFFECTS OF
; FILE REFERENCE: 16153-1637
; CURRENT APPLICATION NUMBER: US/09/095,637D
; CURRENT FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-095-637D-2

Query Match      100.0%; Score 163; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
   |||||
Db 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29

RESULT 14
US-08-481-377-24
; Sequence 24, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE:
;; PCT/US94/00666
;; APPLICATION NUMBER:
;; FILING DATE: 12-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WETHERELL, JR. Ph.D., JOHN R.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: FD2279 PCT
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta 2
;; NAME/KEY: Protein
;; LOCATION: 1..114
US-08-481-377-24

Query Match 100.0%; Score 163; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29
Db 3 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 31

RESULT 15
US-08-491-835-22
; Sequence 22, Application US/08491835
; Patent No. 5821056
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
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;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta 2
;; NAME/KEY: Protein
;; LOCATION: 1..114
US-08-491-835-22

Query Match 100.0%; Score 163; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29
Db 3 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 31

RESULT 16
US-09-153-733A-24
; Sequence 24, Application US/09153733A
; Patent No. 6025475
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/153,733A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/481,377
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 2
; NAME/KEY: Protein
; LOCATION: 1..114
US-09-153-733A-24

Query Match 100.0%; Score 163; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ALDAAAYCFRNVDNCCLRPLYIDFKRDIG 29  
DB 3 ALDAAAYCFRNVDNCCLRPLYIDFKRDIG 31

## RESULT 17

US-08-946-092A-22  
; Sequence 22, Application US/08946092A  
; Patent No. 6030617  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: US  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,092A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/491,835  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr. Ph.D., John R.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: FD3288  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 455-5100  
; TELEFAX: (619) 455-5110  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; CLONE: TGF-beta2  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..114

US-08-946-092A-22  
Query Match 100.0%; Score 163; DB 3; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALDAAAYCFRNVDNCCLRPLYIDFKRDIG 29  
DB 3 ALDAAAYCFRNVDNCCLRPLYIDFKRDIG 31

## RESULT 18

US-09-172-062-22  
; Sequence 22, Application US/09172062  
; Patent No. 6191261  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz

STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/172,062  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,835  
FILING DATE: 23-OCT-1995  
APPLICATION NUMBER: PCT/US94/00695  
FILING DATE: 12-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD3288  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
US-09-172-062-22

Query Match 100.0%; Score 163; DB 3; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAAYCFRNVDNCCLRPLYIDFKRDIG 29  
DB 3 ALDAAAYCFRNVDNCCLRPLYIDFKRDIG 31

## RESULT 19

US-08-624-635-23  
; Sequence 23, Application US/08624635  
; Patent No. 6204047  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: Cunningham, No. 6204047sen  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/624,635  
; FILING DATE: 16-AUG-1996

us-09-822-873-1.open.ra1

Sun Oct 31 14:30:29 2004

```

; Patent No. 6391565
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,705
; FILING DATE: 03-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/153,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-389-705-24

Query Match 100.0%; Score 163; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLVDFKRDIG 29
Db 3 ALDAAACFRNVQDNCCLRLPLVDFKRDIG 31

RESULT 22
PCT-US94-00666-24
; Sequence 24, Application PC/TUS9400666
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: US 08/134,078
; FILING DATE: 08-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; US-08-624-635-23

Query Match 100.0%; Score 163; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLVDFKRDIG 29
Db 3 ALDAAACFRNVQDNCCLRLPLVDFKRDIG 31

RESULT 20
US-09-301-520D-22
; Sequence 22, Application US/09301520D
; Patent No. 6365402
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; FILE REFERENCE: JH1190-3
; CURRENT FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US/09/301,520D
; PRIOR FILING DATE: 1998-10-13
; PRIOR FILING DATE: 1998-10-13
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: PCT/US94/00685
; PRIOR FILING DATE: 1994-01-12
; PRIOR APPLICATION NUMBER: US 08/003,303
; PRIOR FILING DATE: 1993-01-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-301-520D-22

Query Match 100.0%; Score 163; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLVDFKRDIG 29
Db 3 ALDAAACFRNVQDNCCLRLPLVDFKRDIG 31

RESULT 21
US-09-389-705-24
; Sequence 24, Application US/09389705

```



SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/00666  
FILING DATE: 12-JAN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta 2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
PCT-US94-00666-24

Query Match 100.0%; Score 163; DB 5; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29  
|||||  
Db 3 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 31

RESULT 23  
PCT-US94-00685-22  
Sequence 22, Application PC/TUS9400685  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/00685  
FILING DATE: 12-JAN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD3288  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:

CLONE: TGF-beta2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
PCT-US94-00685-22

Query Match 100.0%; Score 163; DB 5; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29  
|||||  
Db 3 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 31

RESULT 24  
US-08-581-529B-20  
Sequence 20, Application US/08581529B  
Patent No. 5770444  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
APPLICANT: Huynh, Thanh  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/581,529B  
FILING DATE: 15-APR-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Lisa A. Haile, Ph.D.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/082001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
US-08-581-529B-20

Query Match 100.0%; Score 163; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 29  
|||||  
Db 4 ALDAAACFRNVQDNCCLRLPLYIDFKRDLG 32

RESULT 25  
US-08-455-559-26  
Sequence 26, Application US/08455559

```

; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JURAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,559
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
; US-08-455-559-26

Query Match 100.0%; Score 163; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.3e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 29
Db 4 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 32

RESULT 26
US-08-525-596B-30
; Sequence 30, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; US-08-525-596B-30

; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,528A
; FILING DATE: 03-Sept-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,670
; FILING DATE: 09-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Halle, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/081001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
; US-08-525-596B-30

Query Match 100.0%; Score 163; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.3e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 29
Db 4 ALDAAFCFRNVQDNCCLRLPYIDFKRDLG 32

RESULT 27
US-08-581-528A-20
; Sequence 20, Application US/08581528A
; Patent No. 5986058
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,528A
; FILING DATE: 03-Sept-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,670
; FILING DATE: 09-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Halle, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/081001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
; US-08-525-596B-30
```



APPLICANT: Huynh, Thanh  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/145,060  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/455,559  
FILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 08/003,144  
FILING DATE: 12-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lisa A. Haile, Ph.D.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/057001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
US-09-145-060-26

Query Match 100.0%; Score 163; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAVCFRNVQDNCCLRLPLYIDFKRDLG 29  
Db 4 ALDAAVCFRNVQDNCCLRLPLYIDFKRDLG 32

RESULT 31  
US-09-378-238-40  
Sequence 40, Application US/09378238  
Patent No. 6465239  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
APPLICANT: McPherson, Alexandra C.  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC  
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN  
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES  
FILE REFERENCE: JHUI120-9  
CURRENT APPLICATION NUMBER: US/09/378,238  
CURRENT FILING DATE: 1999-08-19  
EARLIER APPLICATION NUMBER: 08/795,071  
EARLIER FILING DATE: 1997-02-05  
EARLIER APPLICATION NUMBER: 08/525,596  
EARLIER FILING DATE: 1995-10-25  
EARLIER APPLICATION NUMBER: PCT/US94/03019  
EARLIER FILING DATE: 1994-03-18  
EARLIER APPLICATION NUMBER: 08/033,923  
EARLIER FILING DATE: 1993-03-19  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 40

LENGTH: 115  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: TGF-beta-2  
US-09-378-238-40

Query Match 100.0%; Score 163; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAVCFRNVQDNCCLRLPLYIDFKRDLG 29  
Db 4 ALDAAVCFRNVQDNCCLRLPLYIDFKRDLG 32

RESULT 32  
US-09-629-938-30  
Sequence 30, Application US/09629938  
Patent No. 6500664  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION  
FACTOR-8 AND METHODS OF USING SAME (Amended)  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/629,938  
FILING DATE: 01-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/177,860  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-677-1456  
TELEFAX: 858-677-1465

INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-629-938-30  
Query Match 100.0%; Score 163; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAVCFRNVQDNCCLRLPLYIDFKRDLG 29  
Db 4 ALDAAVCFRNVQDNCCLRLPLYIDFKRDLG 32

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RESULT 33
US-09-686-344-48
; Sequence 48, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-686-344-48

Query Match 100.0%; Score 163; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.3e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
Db 4 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 32

RESULT 34
US-09-412-791D-20
; Sequence 20, Application US/09412791D
; Patent No. 6680372
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: LEE, Se-Jin
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: ANTIBODIES BINDING TO GROWTH DIFFERENTIATION FACTOR-7
; FILE REFERENCE: JHU1130-2
; CURRENT APPLICATION NUMBER: US/09/412,791D
; CURRENT FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/581,528
; PRIOR FILING DATE: 1996-01-09
; PRIOR APPLICATION NUMBER: PCT/US94/07799
; PRIOR FILING DATE: 1994-07-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-412-791D-20

Query Match 100.0%; Score 163; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.3e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
Db 4 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 32
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RESULT 35
US-09-619-061-20
; Sequence 20, Application US/09619061
; Patent No. 6713302
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/619,061
; FILING DATE: 18-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,616
; FILING DATE: 15-JUN-1998
; APPLICATION NUMBER: US 08/581,529
; FILING DATE: 15-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-619-061-20

Query Match 100.0%; Score 163; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.3e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 29
Db 4 ALDAAVCFRNVQDNCCLRPYIDFKRDLG 32

RESULT 36
PCT-US94-00657-26
; Sequence 26, Application PC/TUS9400657
; GENERAL INFORMATION:
; APPLICANT: SE-JIN LEE
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
```

STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/00657  
FILING DATE: 1/12/94  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. PH.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/455-5100  
TELEFAX: 619-455-5110  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
PCT-US94-00657-26

Query Match 100.0%; Score 163; DB 5; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29  
|||||  
Db 4 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 32

RESULT 37  
PCT-US94-07762-20  
Sequence 20, Application PC/TUS9407762  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07762  
FILING DATE: 08-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: TUMARKIN, LISA A., PH.D.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: FD2349  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
PCT-US94-07762-20

Query Match 100.0%; Score 163; DB 5; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29  
|||||  
Db 4 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 32

RESULT 38  
PCT-US94-07799-20  
Sequence 20, Application PC/TUS9407799  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07799  
FILING DATE: 08-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: TUMARKIN, LISA A., PH.D.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: FD-2348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
PCT-US94-07799-20

Query Match 100.0%; Score 163; DB 5; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29  
|||||  
Db 4 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 32

RESULT 39  
PCT-US94-07799-20  
Sequence 20, Application PC/TUS9407799  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07799  
FILING DATE: 08-JUL-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: TUMARKIN, LISA A., PH.D.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: FD-2348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-2  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..115  
PCT-US94-07799-20

Query Match 100.0%; Score 163; DB 5; Length 115;  
Best Local Similarity 100.0%; Pred. No. 7.3e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29

Db 4 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 32  
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RESULT 39  
US-08-132-405-2  
; Sequence 2, Application US/08132405  
; Patent No. 5409896  
; GENERAL INFORMATION:  
; APPLICANT: Ammann, Arthur J.  
; APPLICANT: Rudman, Christopher G.  
; TITLE OF INVENTION: Method of Inducing Bone Growth Using  
; TITLE OF INVENTION: TGF-Beta  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/132.405  
; FILING DATE: 06-OCT-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/063841  
; FILING DATE: 18-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/790856  
; FILING DATE: 12-NOV-1991  
; APPLICATION NUMBER: 07/401906  
; FILING DATE: 01-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 597D1C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-132-405-2

Query Match 100.0%; Score 163; DB 1; Length 414;  
Best Local Similarity 100.0%; Pred. No. 2.8e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29  
|||||

Db 303 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 331  
|||||

RESULT 40  
US-08-395-939A-2  
; Sequence 2, Application US/08395939A  
; Patent No. 5604204  
; GENERAL INFORMATION:  
; APPLICANT: Ammann, Arthur J.  
; APPLICANT: Rudman, Christopher G.  
; TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE  
; TITLE OF INVENTION: GROWTH  
; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/395.939A  
; FILING DATE: 27-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/132405  
; FILING DATE: 12-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/063841  
; FILING DATE: 18-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/790856  
; FILING DATE: 12-NOV-1991  
; APPLICATION NUMBER: 07/401906  
; FILING DATE: 1-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P0597D1C2D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-395-939A-2

Query Match 100.0%; Score 163; DB 1; Length 414;  
Best Local Similarity 100.0%; Pred. No. 2.8e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 29  
|||||

Db 303 ALDAAYCFRNVDNCCLRPLYIDFKRDLG 331  
|||||

RESULT 41  
PCT-US91-01861-2  
; Sequence 2, Application PC/TUS9101861  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Method of Predipositing Mammals to  
; TITLE OF INVENTION: Accelerated Tissue Repair  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US91/01861
; FILING DATE: 19910320
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: U.S. Ser. No. 07/504,495
; APPLICATION NUMBER: 4 April 1990
; FILING DATE: 4 April 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US91-01861-2

Query Match 100.0%; Score 163; DB 5; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29
Db 303 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 331

RESULT 42
PCT-US94-03705-6
; Sequence 6, Application PC/TUS9403705
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; APPLICANT: Mark A. Perrella
; TITLE OF INVENTION: TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR- INHIBITS
; TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
; TITLE OF INVENTION: SYNTHASE GENE
; TITLE OF INVENTION: TRANSCRIPTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03705
; FILING DATE: 5 April 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: Reg. No. 34,819
; REFERENCE/DOCKET NUMBER: 05433/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414
; TYPE: amino acid
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; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-03705-6

Query Match 100.0%; Score 163; DB 5; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29
Db 303 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 331

RESULT 43
5221620-4
; Patent No. 5221620
; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
; GROWTH FACTOR BETA-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/446,020
; FILING DATE: 05-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 285,140
; FILING DATE: 16-DEC-1988
; APPLICATION NUMBER: 234,065
; FILING DATE: 18-AUG-1988
; APPLICATION NUMBER: 148,267
; FILING DATE: 25-JAN-1988
; APPLICATION NUMBER: 106,752
; FILING DATE: 06-OCT-1987
; SEQ ID NO: 4:
; LENGTH: 414
5221620-4

Query Match 100.0%; Score 163; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29
Db 303 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 331

RESULT 44
US-10-017-372E-25
; Sequence 25, Application US/10017372E
; Patent No. 6756215
; GENERAL INFORMATION:
; APPLICANT: Wolfrum, Lawrence A
; APPLICANT: Letterio, John J
; TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
; FILE REFERENCE: 4239-61302
; CURRENT APPLICATION NUMBER: US/10/017,372E
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,292
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 25
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Murine (Mus musculus) TGF-beta2/N-5 FLAG Fusion Construct
US-10-017-372E-25

Query Match 100.0%; Score 163; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.9e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDAAVCFRNVDNCCLRPLYIDFKRDLG 29
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Db      316 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 344
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RESULT 45
US-10-017-372E-27
; Sequence 27, Application US/10017372E
; Patent No. 6756215
; GENERAL INFORMATION:
; APPLICANT: Wolfrain, Lawrence A
; APPLICANT: Lettierio, John J
; TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
; FILE REFERENCE: 4239-61302
; CURRENT APPLICATION NUMBER: US/10/017,372E
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,292
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Murine (Mus musculus) TGF-beta2/N-5 HA Fusion Construct
US-10-017-372E-27
Query Match      100.0%; Score 163; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29
Db      320 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 348
|||||
RESULT 46
5221620-2
; Patent No. 5221620
; APPLICANT: PORCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
; GROWTH FACTOR BETA-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/446,020
; FILING DATE: 05-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 285,140
; FILING DATE: 16-DEC-1988
; APPLICATION NUMBER: 234,065
; FILING DATE: 18-AUG-1988
; APPLICATION NUMBER: 148,267
; FILING DATE: 25-JAN-1988
; APPLICATION NUMBER: 106,752
; FILING DATE: 06-OCT-1987
; SEQ ID NO: 2
; LENGTH: 442
5221620-2
Query Match      100.0%; Score 163; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 29
Db      331 ALDAAYCFRNVQDNCCLRPYIDFKRDLG 359
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Search completed: October 31, 2004, 14:27:17
Job time : 26 secs
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